

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 21, 2005, 23:55:17 ; Search time 373 Seconds
(without alignments)
7198.740 Million cell updates/sec

Title: US-09-943-857A-3

Perfect score: 1641

Sequence: 1 tcgatgaattcacgtggccc.....accgctcttctttgtg 1641

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/prodata/1/ina/5A-COMB.seq:*

2: /cgn2_6/prodata/1/ina/5B-COMB.seq:*

3: /cgn2_6/prodata/1/ina/6A-COMB.seq:*

4: /cgn2_6/prodata/1/ina/6B-COMB.seq:*

5: /cgn2_6/prodata/1/ina/PCTUS-COMB.seq:*

6: /cgn2_6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1248.8	76.1	1650	2	US-08-776-210-6
2	337.8	20.6	1828	3	US-08-362-525-11
3	332.2	20.2	1635	2	US-08-776-210-5
4	264.6	16.1	2045	1	US-08-379-926A-7
5	151.6	9.2	8533	1	US-07-846-181-6
6	151.6	9.2	8533	1	US-07-845-989-6
7	119.6	7.3	1738	2	US-08-932-378A-1
8	75.8	4.6	1572	4	US-09-902-540-2451
9	75.8	4.6	14484	4	US-09-902-540-1108
10	74.4	4.5	1725	4	US-09-810-861B-5
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13	74.4	4.5	2158	4	US-09-949-016-1192
14	74.4	4.5	2158	4	US-09-949-016-1193
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18	74.4	4.5	3016	2	US-08-318-826A-7
19	74.4	4.5	3016	2	US-08-370-156-5
20	74.4	4.5	3016	3	US-08-814-095-5
21	74.4	4.5	3096	2	US-08-318-826A-6
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35 73 4.4 35060 3 US-08-814-095-7
36 72 4.4 2344 3 US-09-347-878-31
37 72 4.4 2734 4 US-09-569-611C-5
38 72 4.4 2781 4 US-09-569-611C-6
39 72 4.4 3018 1 US-08-347-718B-3
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42 72 4.4 3018 6 5200183-1
43 70.2 4.3 2117 4 US-09-949-016-3799
44 70.2 4.3 2169 4 US-09-949-016-555
45 70.2 4.3 2191 4 US-09-595-682B-27

ALIGNMENTS

RESULT 1
US-08-776-210-6
; Sequence 6, Application US/08776210
; Patent No. 5942659
; GENERAL INFORMATION:
; APPLICANT: ALIBERT, Gilbert
; APPLICANT: MOULOUNGUI, Zephirin
; APPLICANT: BOUDET, Alain
; TITLE OF INVENTION: PROCESS FOR PRODUCING FATTY ACIDS OR
; TITLE OF INVENTION: DERIVATIVES THEREOF FROM OLEAGINOUS PLANTS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/776.210
; FILING DATE: 24-JAN-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94 09272
; FILING DATE: 25-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/00957
; FILING DATE: 18-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: IN 387 - BE 6996
; TELEPHONE: 703-521-2297
; TELEFAX: 703-685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1650 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-776-210-6

Sequence 3976, Ap
Sequence 1, Appli
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Sequence 12, Appli
Sequence 12934, A
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Patent No. 5200183
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Sequence 3799, Ap
Sequence 555, App
Sequence 27, Appli

Query Match				76.1%;	Score 1248.8;	DB 2;	Length 1650;
Best Local Similarity				86.2%;	Pred. No. 1.1e-293;	Indels	0; Gaps 0;
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QY	278	TGCTGATGACGTCGAAGTGT	TTCAGGCGGTGCTTCCCGAGAGTGAAGTCCCTCACCA	337			
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QY	338	TCAAAGTGTGCGCGCGCGG	CACCAAGCGCGGCGCCCAACCTCCCGGTCTGCTGGA	397			
DB	344	TCAAAGTGTGCGCGCGCGG	CACCAAGCGCGGCGCCCAACCTCCCGGTGATGCTGGA	403			
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DB	404	TCTTTGGCGGTGGTGTGAGT	GCGTGGTGGCCACGACCATCTTCCCTCCCGCCAGATGATCA	463			
QY	458	CCAAGAGTGTCTATGGCAG	ACATCATCGAGTGGCCCTCAACTACCGTGTGCTT	517			
DB	464	CCAAGAGTGTCTATGGCAG	ACCATCATCGAGTGGCCCTCAACTACCGCGTGTGCT	523			
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DB	524	CGTGGGGTCTTGGCTGTGAG	AGATCAAGCGCGAGGCGAGTGCACACGCGGTTTGA	583			
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RESULT 2

US-08-362-525-11
; Sequence 11, Application US/08362525
; Patent No. 6027910
; GENERAL INFORMATION:
; APPLICANT: KLIS, FRANCISCUS M.
; APPLICANT: SCHREUDER, MAARTEN P.
; APPLICANT: TOSCHKA, HOLSER Y.
; APPLICANT: VERRIPS, CORNELIS T.
; TITLE OF INVENTION: PROCESS FOR IMMOBILIZING ENZYMES TO THE
; TITLE OF INVENTION: CELL WALL OF A MICROBIAL CELL BY PRODUCING A FUSION
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/362,525
; FILING DATE: 04-JAN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 92202080.5
; FILING DATE: 08-JUL-1992
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 92203899.7
FILING DATE: 14-DEC-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/01763
FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 213289/T7020 (V)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1828 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA.
ORIGINAL SOURCE:
ORGANISM: Geotrichum candidum
STRAIN: CMICC 335426
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NAME/KEY: CDS
LOCATION: 40..1731
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FEATURE:
NAME/KEY: sig_peptide
LOCATION: 40..96
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 97..1728
OTHER INFORMATION: /product= "lipase"
OTHER INFORMATION: /gene= "lipb"

US-08-362-525-11

Query Match 20.6%; Score 337.8; DB 3; Length 1828;
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QY 81 TCTCAACGCCATCATCAACGAGGCGTTCTCTCGGCATTCCTTCGCGAGCGCGCGGTGGG 140
DB 141 TGTCTTGAAGGCAAGTTGATACCTTCAAGGGAATCCCATTTGCTGACCCCTCTGTTGG 200
QY 141 CAACCTCCGCTTCAAGGACCTGTGCGGPACTCTGGCTCGCTCAACGGGCCAGAAATTCAAC 200
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QY 201 TTCTTAAGGCGCGCTTTCGATGAGGAGAGAACCCCGAGGGCAGTTT-----246
DB 261 CGACTTCAGCTCTGCTTGTATGACAGCTTGATCTGGCAATGCTTTCTTTGCTTGACAA 320
QY 247 -GAAGAGAACCTTGGCAACGCGCACTCGACTTGTGTATG-----CAGTCAAGGTGT 299
DB 321 AGTAGTGGCTTGGGAAGATTTCTTCTGATTAACCTTAGAGGCCCTCTTTATGACATGGC 380
QY 300 CCAGGCGGTGCTTCCCGAGATGAGGACTCGCTTCACCATCAACGTTGGTGGCGCGCGCGG 359
DB 381 CCAGGGTAGTGTCTCCATGAATGAGGACTGTCTTACCTTAAGTTTCCGCGCCGCTGG 440
QY 360 CACCAAGGGCGGCGCAACCTCCGGTCATGCTCTGGAATCTTTGGCGGTGGGTTTGAGAT 419
DB 441 CACCAAGCGCTGATGTAAAGCTCCCGCTCATGTTTGGATTTACGGTGGTGGCTTTGTGT 500
QY 420 CGGAGCGCCCAACATCTTCCCTCCCGCCAGATGTTCAACGAGAGTGTCTCATCGGCA 479
DB 501 TGGTCTTCTGCTTCTTACCCTGGTAAACGGCTACGTTCAAGGAGAGTGTGGAAATGGCCA 560

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DB 561 GCCTGTGTGTTGTTTTCATCAACTACCGTACCGGCCCTATGATTCCTTGGTGGTGA 620
QY 540 TGACATCAAGGCGGAGGGGAGCGCGGCTTGAAGGACCAAGCGTTTGGGCGATGA 599
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QY 600 GTGGGTGGCAGACAATTTGCGGGTTCGGCGGCGACCCGACCAAGGTGACTATCTTTCG 659
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QY 660 CGAGTCTCGGGCAGCATGTCCGTGTGTGCCACCTCATCTGGAACGACGCGGACAAAC 719
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QY 720 GTAACAAGGCAAGCGGTGTTCCGCGCGGCGCATCATGCACTGTGGAGCCATGGTGGC--- 776
DB 801 CTACAACGGAAGACAGCTTTTCCACTCTGCCATTTCTCAGTCTGGCGTCTCTTCTT 860
QY 777 -----GTCTGACCGGTGGACGCGACGTAAGGCAACGAGATCTACGACCTCTTGTCTC 830
DB 861 CTTTGACTCTACTTCTGTGTCGCGAGTGCCTACAGAGATTTGCTCAGTATGCCGG 920
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DB 981 TGTCTTGACACAGTGGCAGAACTCGTATGATCTTAAGGACCTGTTTGGTCTGCTCCCTCA 1040
QY 945 GCGGTGTCTTATCTCCGCGCGCGCAGCAAGCAATCAACGATGATCATGATCAAGTT 1004
DB 1041 ATTCTTGGATTTGGTCCAGACCGCAGCAACATTTATTCGAGTCCGCTTATGAGCT 1100
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DB 1101 CTACCGCAGCGGTAGATACGCAAGTTTCCCTACATTTACTGGCAACGAGGATGAGGG 1160
QY 1065 CACCATCTTGGGCTCTCTTCTTGAACGTGACCAAGATGCTAGGCGCGGTACTT 1124
DB 1161 TACTATTCTTGGCGCGTGTCTATTAATGCTACCACTACTCCCAATGTTAAGAAGTGGTT 1220
QY 1125 CAAGCAGTCTTTCATCCACGCGCAGCGAGATCGACACCTTGTATGGCGCGTACCC 1184
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QY 1185 CCAGGACATCACCCAGGTTCTCGGTTCCGACACGGGTGTTCTCAACGCGCTCACCCCGCA 1244
DB 1281 CGGCTCTTGGTGGAGGGTTCAACCATTCGCACTGGTATTTCTTAATGCTCTTACCCCTCA 1340
QY 1245 GTTCAAGAGATCTCTGCGGTGCTCGGCGACTTGCATTTCAATCCACGCGCGCGTACTT 1304
DB 1341 GTTCAAGCGCATGTGTGCCATTTTCACTGATTTGTGTTTCCAGTCTCCTCGTGTGTTAT 1400
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DB 1401 GCTTAACGCTACCAAGGACGTCACCGCTGGACTTACCTTGGCCACCCAGCTCCTAATCCT 1460
QY 1362 GTTGCAATCATGGGCACCTTCCATGCAACAGCAATTTGTGGCAGGACTACTTCTTGGG 1421
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QY 1422 AAGCGGAGCGCTCATCAACAACAGCGGTTTATCGGCTTCGCCACCGACTTGGAGCCCAA 1481
DB 1521 TGGGCCATCTTCTGTGTTACCGCGCTACTTATCTCGTTTGCACCAACCCAGACCCCAA 1580
QY 1482 C 1482
DB 1581 C 1581

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US-08-776-210-5
; Sequence 5, Application US/08776210
; Patent No. 5942659
; GENERAL INFORMATION:
; APPLICANT: ALIBERT, Gilbert
; APPLICANT: MOULOUNGUI, Zephirin
; APPLICANT: BOUDET, Alain
; TITLE OF INVENTION: PROCESS FOR PRODUCING FATTY ACIDS OR
; TITLE OF INVENTION: DERIVATIVES THEREOF FROM OLEAGINOUS PLANTS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/776,210
; FILING DATE: 24-JAN-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94 09272
; FILING DATE: 25-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/00957
; FILING DATE: 18-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: IN 387 - BE 6996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-521-2297
; TELEFAX: 703-685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1635 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-776-210-5

Query Match 20.2%; Score 332.2; DB 2; Length 1635;
Best Local Similarity 54.3%; Pred. No. 5.9e-71;
Matches 825; Conservative 0; Mismatches 653; Indels 41; Gaps 6

QY 39 GGTACCCACGCGCAAGCTCGCCAAAGCGGACACCATCACCGTCTCTCAACGCCATCATCAA 98
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QY 264 GACGGCACTCGACTTGGTGATG-----CAGTCCAAGGTGTTCAGGCGGTGCTTCCCA 317
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Db	423	CCCTTGGTAAACGGCTACGTCGAAGGAGAGTGTGAAATGGCGCAGCCTGTGTGTGTGTTTC	482
Qy	498	CGTCAACTACGGTGTCTCCCTCGTGGGGTTCTTGGCTGTGTGATGACATCAAGCCGAGGG	557
Db	483	CATCAACTACCGTACCGTACCGGCCCTTATGATTTCTCGGTGGTGTGATGCCATACCCGTGAGG	542
Qy	558	CAGCGGAAACGCGCGCTTGAAGGACCAAGCGCTTTGGGCATGCGAGTGGGTGGCAGACAACAT	617
Db	543	TAACACCAACGCTGGTCTGCAAGCAGCCAGCGCAAGGCTCTCGAGTGGGTAGCGACAACAT	602
Qy	618	TGCGGGTTTCGGCGCGCACCGGAGCAAGGTGAATACTTTTGGCGAGTCTTGGGGCAGCAT	677
Db	603	TGCCAACTTTTGGTGGTGCATCCGACAAGGTCATGATTTTCGGTGAATCCGCTGGTGCAT	662
Qy	678	GTCCGTCTTGTGGCCACTCATCTGGAACGACGGGCACAACACGTACAAAGGCGAAGCCGTT	737
Db	663	GAGTGTGTCTCACGAGCTTGTGGCTACGGTGTGTGACAACACCTACAACCGAAGAAGCT	722
Qy	738	GTTCGCGCGGGCATCATGAGTCTGGAGCATATGGTGCC-----GTCTGACCCGGT	788
Db	723	TTTTCACTCTGCCATCTTTCAGTCTGGCGGTCTCTTCTCTTACTTTTGACTCTACTTCTGT	782
Qy	789	GGACGGCACGTACGGCAACGAGATCTACGACCTCTTTGTCTCGAGTCTCGCTGTGCGAG	848
Db	783	TGTTCCGAGAGTGCCTACAGCAGATTTGCTCAGATATGCCGGAATGATGCCAGCGCCAG	842
Qy	849	CGCCAGCGACAAGCTCGCGTGTCTTGGCAGTGGGTCTPAGCGACAACCTTGTCTGATGCCAC	908
Db	843	TGACATGAATAACTCTGCGTTGTCTCCGACAGATCCAGCGATGCTCTTGACAGTGCACA	902
Qy	909	CAAC-----AACACTCTCGGGTTCTTGGCGTACTCTCTGTTGGGTTGTCTTATCTCC	961
Db	903	GAACTGTACGATCTCAAGGACCTGTTTGGCTGTCTCCCTCAATTCCTTGGATTTGTGTCC	962
Qy	962	CGCGGCCGAGCGGCAAGAACATCACCGATGACATGTACAAGTTGGTTCGCGCAGCGCAAGT	1021
Db	963	C-AGACCCGAGCGCAACATTTATTCGATGCCGCTTATGAGCTCTACCGCAGCGGTAGAT	1021
Qy	1022	ATGCAAGCGTTCCGTTGATCATTTGGCGACACAGAACGACGAGGGCACATCTTTGGGCTCT	1081
Db	1022	ACGCCAAGTTCCCTACATTTACTGTTAACTGTTAACTGAGGATGAGGGTACTATTCTTTGCCCCCG	1081
Qy	1082	CTTCTTTGAAGTGAACCAAGATGCTCAGGCCGCTGTACTTACTTCAAGCAGTCTTTTCATCC	1141
Db	1082	TTGCTATTAAATGTACACAGACTCCCATGTTAAGAAAGTGGTTGAAGTACATTTGTAGCG	1141
Qy	1142	ACGCACGACGCGGAGATCGACACCTTGTATGGCGGTACTCCCCAGGACATCACCCAGG	1201
Db	1142	AGGCTTCTGACGCTTGCGTTGATGCTGTTTTTGTGCTCTACCCCGGCTCTTGGTCGAGG	1201
Qy	1202	GTCTCTCGTTTCGACAGGGTGTCTCAACGCCCTCACCCCGCAGTTTCAAGAGATCTCTG	1261
Db	1202	GTGCGCATTTCCGACATGGTATTTCTTAATGCTCTGACGCCCTCAGTTTCAAGCGCATTCGCTG	1261
Qy	1262	CGGTGCTCGGACCTTGCATTTCAATCCACGCCGCCCTACTTCTCTCAACCACTTCCAGG	1321
Db	1262	CCATTTTCACTGATTTGCTGTTCCAGTCTCCTGTCGTGTTATGCTTAAACGTACCAAGG	1321
Qy	1322	CGCGCACCAAGTACTCGTTCTCTTAAAGCAGTCTCTCT---GGGTGCGCAATCATGGGCA	1378
Db	1322	ACGTCAACCGCTGACATTTACTTGGCAACCGAGTCCATAACCTCGTTTCCATTTTGGGTA	1381

RESULT 5

US-07-846-181-6
 ; Sequence 6, Application US/07846181
 ; Patent No. 5360732
 ; GENERAL INFORMATION:
 ; APPLICANT: BERKA, RANDY M
 ; APPLICANT: FOWLER, TIMOTHY
 ; APPLICANT: REY, MICHAEL W
 ; TITLE OF INVENTION: PRODUCTION OF ASPERGILLUS NIGER
 ; TITLE OF INVENTION: CATALASE-R
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: GENENCOR INTERNATIONAL, INC.
 ; STREET: 180 KIMBALL WAY
 ; CITY: SOUTH SAN FRANCISCO
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/846,181
 ; FILING DATE: 19920304
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: HORN Ms, MARGARET A
 ; REGISTRATION NUMBER: 33401
 ; REFERENCE/DOCKET NUMBER: GC204-151
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-742-7536
 ; TELEFAX: 415-742-7217
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; TYPE: NUCLEIC ACID
 ; LENGTH: 8533 base pairs
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-07-846-181-6

Query Match 9.2%; Score 151.6; DB 1; Length 8533;
 Best Local Similarity 53.5%; Pred. No. 8.5e-27;
 Matches 590; Conservative 0; Mismatches 484; Indels 28; Gaps 12;

QY	322	GAGGACTGCTCACCATCAACGTGGTGGCGCGCGCGGACCAAGCGGCGCGCCACCTC	381
DB	12	GAGGATTGTCTGAACATTGACATTCGGCGCGCGCGGACCCCAACTGCGGCGCAATGC	71
QY	382	CGGTCATCTCTGGATCTTTGGCGGTGGTTGAGATCGGCGAGCGCCACCATCTTCCCT	441
DB	72	CCGTGCTGCTCGGATCTTTGGCGGAGCCTTGAACCTGGTTCAAGGCCATGTATGAC	131
QY	442	CCGCGCCAGATGGTCAACCAAGATGTGCTCATGGGCAAGCATCATCACTCGCGCGTC	501
DB	132	GGCAACCAACGATGGTATCATCGTCGATAGACAAGATATGCCATCTGCTGTTAGCGATG	191
QY	502	AACTACCGTGTGCTCGTGGGGTCTTGGCTGGTGGATGACATCAAGCCGAGGCGAGC	561
DB	192	AACTATCGGTAGGGGGCTTCGGGTTCTGCCCGAAGAGGATTTCTGGAGGACGGTCC	251
QY	562	GGGAACCGCGGCTTGAAGACCAAGCGCTTTGGGCATGTCAGTGGGTGGCGAGACAATGCC	621
DB	252	GCCAACTTAGG--TCTTTGACCAAGCCTTGCC--TAGTGGGTGGCGCAACATCGAG	306
QY	622	GGGTTCCGGCGGACCCGAGCAAGTGACTATCTTTGGCGAGTCTGGCGGCGAGCATGCC	681
DB	307	GGGTTTGGTGGAGACGAGA--CAAGGTGACAATCTGGGGAGAAATCAGCAGGGGCTATTTCT	365

QY	682	GTGTTGTCCACCTCATCTGGAAACGACGCGGACACACGTAACAAGGCAAGCGTGTGTC	741
DB	366	GTCTTTGATCAGATGATCT--GTACACGGAACATCGCTTACAGGAACAAGCCCTTGT	423
QY	742	CGCGCGGCATCATGACGATCTGGAGCCATGGTCCGCTCTGACCCCGTGGACGGCACGTAC	801
DB	424	CG--GGAGCCATCATGACTCCGGT--ATGTGTTCCGCGAGACCCTCTCGACGGGTCAAGG	481
QY	802	GGCAACGAGATCTACGACCTCTTTCTCTCGAGTGTGGCTGTGGCAGCGCCGACGACAAG	861
DB	482	GATCAGCAAGTATATGATGCGGTCTGGACTCTGCGAGCTGTCTCTTCCAAACGACACC	541
QY	862	CTCGCGTCTTGGCGAGTCTAGCGACCTTGTCTCGATGCGACCAACAACACTCTCT	921
DB	542	CTGGCTTGTCTGCGTGAAGTACACCGACTATCTCAATGCGGCAAACTCTGTCGCGG	601
QY	922	GGGTTCTTGGCGTACTCTCGTTGGGTTGTCTTATCTCCCGCGCGCCGACGGCAAGAAC	981
DB	602	GGATCTAGTTATCACCG--TGGCGCTATCATATGTCCTCGACGACGAGGAGCGCA	658
QY	982	ATCACCGATGACATGTAACAAGTTGGTGGCGGACGCAAGTATGCAAGGTTCCCGTATC	1041
DB	659	TTTGTGCGCGTC--GCCAGATTTTGGGTAAGCAGGGAAGTATGCGCGGTCCCATTCATC	717
QY	1042	ATTGCGGACCAAGACGAGGCGACCATCTTTGGGCTCTCTTCTTGAACGTGACCAAG	1101
DB	718	GTGGCGGACCAAGAGGATGAGGGGACC--TTGTTGCGCTTGTGTTTACGTCTTACGACGATC	776
QY	1102	AATGCTCAGGCGCGTCTTACTTCAAGCAGTCTTTTATCCAGCGGACGCGGAGATC	1161
DB	777	GACGAGGTAGTCGACTATCTGGGCACCTACTTCTTATGACGCTAGCCAGGAGCAGCTT	836
QY	1162	GACACTTGTATGGCGGCGTACCCCGAGGACATCACCCAGGTTCTTCCGTTGACACGGGT	1221
DB	837	GAAGAAATTTAGTGGCGCTGTACCCAGACACCAATATATGAGTCTTCCCTTACGACGCGGC	896
QY	1222	GTCTCTCAACGCGCTCACCCCGCGAGTTCAAGAGAATCTCTGGGTCTCGGCGACCTTGA	1281
DB	897	AGGC--CAACAACTGGTATCCGCAATTTAAGCAATTTGGCGCGCATTTCTCGGCGACTTGGTC	955
QY	1282	TTTCATCCACGCGCGCGCTACTTTC-----CTCAACCACTTCCAGGCGCGCACCA	1330
DB	956	TTTACCAATTTACCGCGCGCATTTCTGTCATATGACAGGAGCTCTCCCTGACCTCCCGA	1015
QY	1331	AGTACTGTTCTCTTAAGCAGCTCTCTGGTGGTCCCAATCATGGGCGACCTTCCATGCA	1390
DB	1016	AATGTCGTACTCTGGCGACCTATGACTAT--GGCAGCCAATTTGGGGGACCTTCCATGGAA	1074
QY	1391	ACGACATTTGTGGCAGGACTA 1412	
DB	1075	GTGACCTCTGAGGTGTTCTA 1096	

RESULT 6

US-07-845-989-6
 ; Sequence 6, Application US/07845989
 ; Patent No. 5360901
 ; GENERAL INFORMATION:
 ; APPLICANT: BERKA, RANDY M
 ; APPLICANT: FOWLER, TIMOTHY
 ; APPLICANT: REY, MICHAEL W
 ; TITLE OF INVENTION: PRODUCTION OF ASPERGILLUS NIGER
 ; TITLE OF INVENTION: CATALASE-R
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: GENENCOR INTERNATIONAL, INC.
 ; STREET: 180 KIMBALL WAY
 ; CITY: SOUTH SAN FRANCISCO
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk


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; MOLECULE TYPE:  cdna
; FEATURE:
; NAME/KEY:  CDS
; LOCATION:  11..1726
US-08-932-376A-1

```

Query Match	7.3%	Score 119.6	DB 2	Length 1738
Best Local Similarity	53.8%	Pred. No.2.8e-19		
Matches 301	Conservative 0	Mismatches 244	Indels 15	Gaps 2
Qy	322	GAGGACTGCCTCACCATCAACGTCGGTCGGCGCGCGGACCAAGGCGGGCGCCAAACCTC	381	
Db	371	GAGGATTGCCCTCTTCCTCAATGTCGTTGCCCGCGCGCTCGTCGAGAGGGCGACATCTT	430	
Qy	382	CCGGTCATGCTCTGGATCTTTTGGCGGTGGGTTTGAGATCGGACGCCCCACCATCTTCCCT	441	
Db	431	CCGTCCTCGTCTACATTTCACGGAGGTGGCTACGCCCTCGGCGATCGAGCACCGGCAGC	490	
Qy	442	CCGCGCCAGATGGTACCAAGAGTGTCTCATGSGGCAAGCACATCATCCAGTGGCCGCTC	501	
Db	491	GACTTTGCCGCTTCACCAA-----GCACACGGGACCAAGATGGTCTGTGTTAAATCTC	544	
Qy	502	AATACACGCTGTGCCTCGTGGGGGTTCTTGCGCTGGTGATGACATCAAGCGCGAGGCGAGC	561	
Db	545	CAGTACCGTCTCGCAGCTTTGGTTTCTCGCTGGCCAGCCATGAAGGACTACGGTGTA	604	
Qy	562	GGGAAACCGCGCTTGAAGGACCGAGCTTTGGGCAATGCAGTGGGTGGCAGACAACTTGCC	621	
Db	605	ACGAACCGCGCTTGTCTTGACCAAGCAATTCGCCCTTCAATGGGTTCACAGCACGTCTCG	664	
Qy	622	GGGTTCCGCGCGGACCCGAGCAGAGTGACATCTTTGGCGAGTCTGGGCGCAGATGTC	681	
Db	665	AAGTTCGGCGGCAACCCCGATACAGTTACGATTTGGGGCGAGTCTGCAGGCGCAGGCTCC	724	
Qy	682	GTGTTGTGCCACCTCATCTGGAACGACGGGCAACACACGTACAAGGC-----AAG	732	
Db	725	GTTATGAACACAGATCATTGCMAACGGCGGCAACACCGTCAAGGCTCTCGGTCTCAAGAAG	784	
Qy	733	CCGTTGTTCCGCGGGGCGATCATGCAGTCTGGAGCCATGGTGGCGTCTGACCCGGTGGAC	792	
Db	785	CCCCTCTTCCACGCTGCATCGGCTCTCTCGCTCTTCTCCCTACCAAGCAAGTACAAC	844	
Qy	793	GGCAGCTACGGCAACGAGATCTACGACCTCTTTGCTCTCGAGTGTGCTGTGGCAGCGCC	852	
Db	845	TCGCCCTTCGCGAGCTGCTCTACTCCAACTCGTCTCGGGCAAAACTGCACCAAGGCC	904	
Qy	853	AGCGACAAGCTCGCGTGCTT	872	
Db	905	GCCTCGTCCTCGCTTGCTT	924	

RESULT 8

```

US-09-902-540-2451
; Sequence 2451, Application US/09902540
; Patent No. 683447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 2451
; LENGTH: 1572
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-2451

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Query Match	4.6%;	Score 75.8;	DB 4;	Length 1572;
Best Local Similarity	52.3%;	Pred. No. 1.2e-08;		
Matches 192;	Conservative	0;	Mismatches 172;	Indels 3; Gaps 1;

Qy	336	CATCAAGTGGTGGGCGCGGGCCACCAAGGCGGGCCCAACCTCTCCCTCCGCCCCAGATGGT	395
Db	261	CTTCCTCAATGTGTGGACGCCCAAGCTGGATGCGGGCGGAAGCTGCCGTGGTGTCTG	320
Qy	396	GATCTTTGGCGGTGGGTTTGAGATCGGCAGCCCCACCATCTTCCTCCGCCCCAGATGGT	455
Db	321	GATTCAGGCGGCGCCTTCTCATCGCTCGGCGCGTCTGCCGCCCTATGAAGGATTC	380
Qy	456	CACCAAGAGTGTGTCATATGGGCAAGCACATCATCAGTGGCGGTCAACTACCGTGTTC	515
Db	381	TTTGGCGTCGCGGACGCTGTGTGTGTGACTTCACTACCGCTCGGGGCACC--TGGG	437
Qy	516	CTCGTGGGGGTTCTTGGCTGGTATGACATCAAGGCGGAGGCGAGCGGGAACCGCGCTT	575
Db	438	CTTCTTCATGCATCCGCGCGCTGGAGAAGGAGAATCCGGGTGGGCGCCGCAACTTCGCGCT	497
Qy	576	GAAGGACCAAGCTTTGGGCATGCAGTGGGTGGGAGACAACTTTCGCGGGTTCCGGCGGCGA	635
Db	498	GCTGGACCAAGTCTGGCGCTGGAATGGGTGCGGACAACTATCGCGGTTTCGGCGGCGA	557
Qy	636	CCGAGCAAGGTGACTATCTTTGGCGAGTCTCGGGGAGCATGTCGTGTGTGTGCGCACCT	695
Db	558	CCCGGCAATGTCAACGTGTATGGGACAGTTCGGGCGGCGCCCAAGAGGTCTCTGTGCTCTT	617
Qy	696	CATCTGG 702	
Db	618	CACGTGC 624	


```

RESULT 9
US-09-902-540-1108/c
; Sequence 1108, Application US/09902540
; Patent No. 683347
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1108
; LENGTH: 14484
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(14484)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1108

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	Query Match	4.6%	Score 75.8	DB 4	Length 1484	
	Best Local Similarity	52.3%	Pred. No. 2.7e-08			
	Matches 192	Conservative 0	Mismatches 172	Indels 3	Gaps 1	
Qy	336	CATCAACGTGGTCGCGCCGCCGGGCACCAGGCGGCGGCCAACCTCCCGGTCAATGCTCTG				395
Dd	11268	CTTCTCAATGTGTGACGCCCAAGCTGGATCGGGCGGAAGCTGCCGTGGTGTTCTG				11200
Qy	396	GATCTTTGGCGGTGGTTTGAGATCGCAGCCCCACAATCTTCCTCCCGCCAGATGGT				455
Dd	11208	GATTACGGCGGCGCCTTCGTATCGCTCGGSCCGTCTGCCGCCCTATGAAGGGATTCA				1114
Qy	456	CACCAAAGATGTCTCATGGGCAAGCACATCATCCAAGTGGCCGTCAACTACCGTGTTC				515


```
Db 746 GCGGGGCTGTTCACAGGGCGTGTCTGACAGCGGTGCCCCCAATGAGACCTTGGGCCA 805
Qy 770 TGGTGGCTGTGACCGGTGGAGCGGACGCTACGGCAACAGAGATCTACGACCTTTGTCT 829
Db 806 CGTGGGATGGAGAGGCCCTGCGAGG---GCCACGAGCTGGCCACCTTTGGGCT 862
Qy 830 CGAGTCTGGCTGTGACAGCGCGCAGCAAGCTCGCGTCTTTGCGAGTGGCTTAGCG 889
Db 863 GTCCTCAGGCGGCACTGGTGGGAATGACACAGAGCTGGTAGCCTCGCTTCGACACGAC 922
Qy 890 ACACCTTGTCTGATGCCACCAACACTCTCTGGGTTCTTGGGTAATCTCTCTGGTGGT 949
Db 923 CAGCGAGGTCTCTGTGTGAACCAAGATGGCAGCTGCTCTCAAGAAAGCGTCTTCGGT 982
Qy 950 TGTCTTATCTCCCGCGCGCGGCAAGCAATACACCATGACATGTACAAGTTGGTGC 1009
Db 983 TCTCTTCTGCTGTGTAGATGGAGACTTCTCAGTGACACCCAGAGGCCCTCATCA 1042
Qy 1010 GCGACGGCAAGTATGCAAGGTTTCCCGTGTATCATTTGGCGACAGACGAGGGCACCA 1069
Db 1043 ACGCGGAGACTTCCACGGCGCTGCAGTGTCTGTGGTGTGGTGAAGATGAGGCTCGT 1102
Qy 1070 TCTTTGGGCTCT 1081
Db 1103 ATTTTCTGTTT 1114

RESULT 13
US-09-949-016-1192
; Sequence 1192, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1192
; LENGTH: 2158
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1192

Query Match 4.5%; Score 74.4; DB 4; Length 2158;
Best Local Similarity 47.1%; Pred. No. 2.9e-08;
Matches 373; Conservative 0; Mismatches 401; Indels 18; Gaps 4;
Qy 290 CCAAGGTGTTCCAGGGGTGCTTCCCGAGTGAGGACTGCTCACCATCAACGTGGTGC 349
Db 435 CCGAGATGTGAAACCCCAACCGTGAGCTGAGCGAGGACTGCTGTACCTCAAC---GTGT 491
Qy 350 GCGCGCGCGGCACCAAGGGCGGCAACCTCCCGTCAATGCTCTGGATCTTTGGCGGTG 409
Db 492 GGACACCATACCCCGGCTTACATCCCGCACCCCTGTCTCTGTGATCTATGGGGTG 551
Qy 410 GGTGTTAGATCGGCGGCCCAACCATTTCTCCCTCCCGCCAGATGGTCAACAGAGTGTGC 469
Db 552 GCTTCTACAGTGGGGCTCTCTCTTGGACGTGTACAGTGGCGCTTC-----TTGG 602
Qy 470 TCATGGGCAAGCACATCATCCAGTGGCGCGTCACTACCGTGTGCTGCGGGGTTCT 529
Db 603 TACAGGCCGAGAGGACTGTGTGTTGTTCCATGAACCTACCGGTGGGAGCCTTTGGCTTCC 662
Qy 530 TGGCTGGTGTATGACATCAAGGCGGAGGCGAGCGGGAACGCGCGCTTTGAAGGACGCGTT 589
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Db 663 TGGCCCTGCGGGGAGC---CGAGAGGCCCGGCAATGTGGTCTCTCTGGATCAGAGC 719
Qy 590 TGGGATGAGTGGGTGGAGACAATTCGCGGGTTTGGCGGCGACCCGAGCAAGGTGA 649
Db 720 TGGCCCTGAGTGGGTGGAGAGACGTTGGCAGCCTTGGGGGTGACCCGACATCAGTGA 779
Qy 650 CTATCTTTGGGAGTCTCGGCGACATGTCGCTGTGTCGACCTCATCTGGAACGAGC 709
Db 780 CGCTGTTTGGGAGAGCGCGGAGCCGCTCGGTGGGATGACCTGTGTCTCCCGCCCA 839
Qy 710 GCGACAACACGTACAAAGGCAAGCGTTGTTCCGCGCGGCGCATATGACAGTCTGGAGCCA 769
Db 840 GCGGGGCTGTTCACAGGGCGGTGTCAGAGCGGTGCCCCCAATGGAACCTTGGGCCA 899
Qy 770 TGGTCCGCTGTACCCCGTGGAGCGACGTACGGCAACAGATCTACGACCTCTTTGTCT 829
Db 900 CGGTGGGATGGGAGAGGCCCGTTCGACG---GCCACGAGCTGGCCACCTTTGGGCT 956
Qy 830 CGAGTGTGGCTGTGGCAGCGCCAGCAAGCTCGCGTGTGCGAGTGGCTGTAGCG 889
Db 957 GTCCTCCAGGCGGCACTGTGTGGATGACACAGACTGTAGCTGCTTCGACACGAC 1016
Qy 890 ACACCTTGTCTGATGCCACCAACACTCTCTGGGTTCTTGGCGTACTCTCTGTCGCT 949
Db 1017 CAGCGCAGGTCTCTGTGAACCAACGAGTGCACGTCTGCTCAAGAAAGCGTCTTCGCT 1076
Qy 950 TGTCTTATCTCCCGCGCGCGGCAAGCAATCACCAGTACCATGATGATGATGATGATG 1009
Db 1077 TCTCTCTGCTGTGTAGATGGAGACTTCTCAGTGACACCCAGAGGCCCTCATCA 1136
Qy 1010 GCGACGGCAAGTATGCAAGCGTTCCCGTGTATCATTTGGCGACAGCAACGAGGGCACCA 1069
Db 1137 ACGCGGAGACTTCCAGGCGCTGCAGGCTGTGGTGTGGTGAAGATGAGGCTCGT 1196
Qy 1070 TCTTTGGGCTCT 1081
Db 1197 ATTTTCTGTTT 1208

RESULT 14
US-09-949-016-1193
; Sequence 1193, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1193
; LENGTH: 2158
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1193

Query Match 4.5%; Score 74.4; DB 4; Length 2158;
Best Local Similarity 47.1%; Pred. No. 2.9e-08;
Matches 373; Conservative 0; Mismatches 401; Indels 18; Gaps 4;
Qy 290 CCAAGGTGTTCCAGGGCGGTGCTTCCCGAGAGTGGAGTGTCTCACCATCAACGTGGTGC 349
Db 435 CCGAGATGTGAAACCCCAACCGTGAGCTGAGCGAGGACTGCTGTACCTCAAC---GTGT 491
```

350 GGCCGCGCGGACCAAGCGCGGCGCAACCTCCCGTCTATGCTCTGGATCTTTGGCGGTG 409
492 GGACACCATACCCCGGCTCATCCCCACCCCTGCTCTCTGGATCTATGGGGTG 551
410 GGTGTTAGATCGGAGCGCCACATCTTCCCTCCCGCCAGATGTCACCAAGATGTGC 469
552 GCTTCTACAGTGGGGCTCTCTTGGACGTGACGATGGCGGCTTC-----TTGG 602
470 TCATGGGCAAGCACATCATCCAGTGGCGGCTCACTACCGTGTGTGCTGTGGGGTCTT 529
603 TACAGGCCAGAGGACTGTGCTGTGTGTCATGAACCTACCGGTGGGAGCTTTGGCTTCC 662
530 TGGCTGCTCATGACATCAAGGCGGAGGCGAGCGGAAACCGCGCTTTGAAGGACCAAGCTT 589
663 TGGCCCTGCGGGGAGC---CGAGAGGCCCGGGCATGTGGGTCTCTGGATCAGAGGC 719
590 TGGGATGTCAGTGGGTGGGAGCAAAATTCGCGGGTTCGGCGGCGACCCGAGCAAGGTGA 649
720 TGGCCCTGCACTGGGTGGGAGGAGACGTGGCAGCCTTCGGGGGTGACCCGACATCAGTGA 779
650 CTATCTTTGGCAGTCTGGGCGAGCATGTCGTTGTTGGCCACCTCATCTGGAACGAGG 709
780 CGCTGTTTGGGAGAGCGCGGGAGCGCCTCGGTGGGCATGCACCTGTGTCGCCGCCCA 839
710 GCGACAAACGCTACAGGCAAGCCGCTGTTCCGCGCGGCGCATGCAAGTCTGGAGCCA 769
840 GCGGGGCTGTTTCACAGGCGGTGCTGACAGAGCGGTGCCCCCAATGGACCTTGGGCCA 899
770 TGGTGCCTGCTACCCCGGTGAGCGGACGTCAGCGCAACGAGATCTACGACCTCTTTGTCT 829
900 CGGTGGGATGGAGAGGCGCTGCGCAGG---GCCACGAGCTGGCCCAACCTTGTGGGT 956
830 CGAGTCTGCTGTGGCAGCGGCGGAGCAAGCTCGGTGCTTGGCGAGTGTCTAGGG 889
957 GTCTCCAGGCGGCACTGGTGGGAATGACACAGAGCTGTGAGCTGCTTCGGACACGAC 1016
890 ACACCTTGTCTGATGCCACCAACACACTCTCTGGGTTCCTGGCGTACTCTCTGTGGCT 949
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RESULT 15
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; Sequence 5, Application US/08318826A
; Patent No. 5891725
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Eckstein, Fritz
; TITLE OF INVENTION: Synthetic Antisense
; TITLE OF INVENTION: Oligodeoxynucleotides and Pharmaceutical Compositions
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Kohn & Associates
; STREET: 30500 No. 5891725thwestern Hwy., Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: US
; ZIP: 48334
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,826A
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: 2391.00001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (248) 539-5050
TELEFAX: (248) 539-5055
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2256 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: /note= "Splice variant: Exons 1, 2,
OTHER INFORMATION: 3, 4 and 6"
US-08-318-826A-5
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 Job time : 377 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Run on: September 22, 2005, 00:44:42 ; Search time 1746 Seconds
(without alignments)
6284.070 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	895	54.5	1511	10	US-09-943-857-9
5	888	54.1	1650	24	US-11-061-894-1
6	888	54.1	1650	24	US-11-061-233-1
7	778.4	47.4	1469	10	US-09-943-857-1

8	354.2	21.6	1687	17	US-10-369-493-27923	Sequence 27923, A
9	119.6	7.3	1716	9	US-09-801-852A-1	Sequence 1, Appli
10	103.8	6.3	1727	17	US-10-369-493-41665	Sequence 41665, A
11	98.4	6.0	1419	17	US-10-369-493-34501	Sequence 34501, A
12	74.4	4.5	1725	9	US-09-810-861B-5	Sequence 5, Appli
13	74.4	4.5	1725	22	US-10-792-491-5	Sequence 5, Appli
14	74.4	4.5	2509	21	US-10-887-553A-108	Sequence 108, App
15	74.4	4.5	5767	9	US-09-810-861B-3	Sequence 3, Appli
16	74.4	4.5	5767	22	US-10-792-491-3	Sequence 3, Appli
17	74.4	4.5	14446	9	US-09-810-861B-4	Sequence 4, Appli
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20	73.6	4.5	2350	21	US-10-741-600-401	Sequence 401, App
21	73.6	4.5	2428	9	US-09-969-347-220	Sequence 220, App
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40	69	4.2	1728	18	US-10-451-168-40	Sequence 40, Appl
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42	69	4.2	1746	13	US-10-023-515-3	Sequence 3, Appli
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ALIGNMENTS

RESULT 1
US-09-943-857-3
; Sequence 3, Application US/09943857
; Publication No. US20030124701A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Jai-Fu
; APPLICANT: Lee, Guan-Chiun
; APPLICANT: Tang, Shye-Jye
; TITLE OF INVENTION: RECOMBINANT CANDIDA RUGOSA LIPASES
; FILE REFERENCE: 08919-066001
; CURRENT APPLICATION NUMBER: US/09/943.857
; CURRENT FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1532
; TYPE: DNA
; ORGANISM: Candida rugosa
US-09-943-857-3

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Best Local Similarity	94.5%	Pred. No. 0;		
Matches 1505;	Conservative	0;	Mismatches 25;	Indels 62;
Gaps	16;			
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; Sequence 9, Application US/09943857
; Publication No. US20030124701A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Jai-Fu
; APPLICANT: Lee, Guan-Chiun
; APPLICANT: Tang, Shye-Jye
; TITLE OF INVENTION: RECOMBINANT CANDIDA RUGOSA LIPASES
; FILE REFERENCE: 08919-066001
; CURRENT APPLICATION NUMBER: US/09/943,857
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1511
; TYPE: DNA
; ORGANISM: Candida rugosa
US-09-943-857-9
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Best Local Similarity 83.0%; Pred. No. 5.7e-243;
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QY 224 AGCAGAACCCCGAGGCGCACGTTTGAAGAGAACTTTGGCAAGACGGCACTCGACTTGGTGA 283
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QY 284 TGCAGTCAAGGTGTTCAGCGGTGTCTCCCGAGAGTGAGGACTGCTCTACCATCAACG 343
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 Db 1643 TCGT 1646

RESULT 6

US-11-061-233-1
 ; Sequence 1, Application US/11061233
 ; Publication No. US20050198706A1
 ; GENERAL INFORMATION:
 ; APPLICANT: McCutchen, Billy F.
 ; APPLICANT: Abad, Andre R.
 ; APPLICANT: Wong, James F.

; APPLICANT: Yu, Guo Cao
 ; TITLE OF INVENTION: Lipases and Methods of Use
 ; FILE REFERENCE: 035718/286811
 ; CURRENT APPLICATION NUMBER: US/11/061,233
 ; CURRENT FILING DATE: 2005-02-18
 ; PRIOR APPLICATION NUMBER: 60/546,605
 ; PRIOR FILING DATE: 2004-02-20
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 1650
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic lipase from C. cylindracea; ctd codon
 ; OTHER INFORMATION: substitution for proper expression in plants
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(1650)
 US-11-061-233-1

Query Match 54.1%; Score 888; DB 24; Length 1650;
 Best Local Similarity 71.7%; Pred. No. 5.6e-241;
 Matches 1164; Conservative 0; Mismatches 460; Indels 0; Gaps 0;
 QY 17 GCCCAGCGCGCGTCTCGGATCGGTACCCACGCGCAAGCTGCCAACCGCGACACCATCA 76
 Db 23 GCCTCATCGCCAGCGTCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC 82
 QY 77 CCGGTCTCAACGCCCATCATCAACGAGCGGTTCCTCGGCATTCCTTTGCCAGCGCGCGG 136
 Db 83 CCGGCTCAACGCCCATCATCAACGAGCGCTTCTCTGGCATCCCGTTCCCGAGCGCGCGG 142
 QY 137 TGGGCAACCTCGCTTTAAGGACCTCTGTGCGTACTCTGTGCTGCTCAACGGCGCAAGT 196
 Db 143 TCGGCAACCTCGCTTTAAGGACCTCGGTCCCGTACAGCGCGAGCCTCGACGGCGCAAGT 202
 QY 197 TCACCTTCTTACGCGCGCTTTCATGACAGCAGAACCCCGAGGCGACGTTTGAAGAGAAC 256
 Db 203 TCACAGCTACGCGCGGAGCTGATGACAGCAGAACCCCGAGGCGACCTACGAGGAGAAC 262
 QY 257 TTGGCAAGCAGCGCATCTGACTTTGGTGTGATGTCAGTCCAAAGGTGTTCCAGCGGTGTTCC 316
 Db 263 TCCGGAAGCGCGCTTCGACCTCGTCATGACAGCAGCAAGTCTTCGAGCGCGTCAGCCGA 322
 QY 317 AGATGAGGACTGCTTACCATCAACGTGTGCGCGCGCGCGGACCAAGCGGGCGGCA 376
 Db 323 GCAGCGAGGACTGCTTACCATCAACGTGCTGCGCGCGCGCGGACCAAGCGCGCGGCA 382
 QY 377 ACCTCCCGGTCACTGCTTGGATCTTTGGCGGTGGTGTGAGATCGGACGCCCACTCT 436
 Db 383 ATCTGCTGTGATGCTGTGGATATTCGGGGGGGCTTCGAAAGTGGAGGCACTCGACGT 442
 QY 437 TCCCTCCCGCGCAGATGTCACCAAGAGTGTGCTCATGGGCAAGCACAATCACTCCAGTGG 496
 Db 443 TCCCGCGCGCAATGATACAAAGTCTATAGCGATGGGGAAGCAATAATACAGTCT 502
 QY 497 CGGTCAACTACGTTGCTTCCCTGCTGGGGGTTCCTGGCTGGTGTGATGACATCAAGCGGAGG 556
 Db 503 CAGTCAATTAACAGGTCAGTGTGGGTCTTCTCGCTGGAGATGAAATCAAAAGCAGAGG 562
 QY 557 GCAGCGGAACCGCGGCTTGAAGGACACGAGCTTTGGGATCGAGTGGGTGGCAGACAACA 616
 Db 563 GCTCCGCAATGCGGGTTGAAGATCAAGCTTGGTATGCAATGGGTGGCTGATATA 622
 QY 617 TTGCGGGTTCGGCGCGACCCGAGCAAGGTGACTATCTTTGGCGAGTCTGCGGCGAGCA 676
 Db 623 TTGCAGCCTTTGGAGCGGATCCTACTAAAGTCAACCATATTTGGGSAATCGCGGGTCTTA 682
 QY 677 TGTCCGTGTTGTGCCACCTCATCTGGAAACGAGCGGCGACAACCGTACAAAGGCAAGCGGT 736
 Db 683 TGTCAATTATGTGTGCATCTCTATGGAAACGAGGAGATAATACGTACAAAGCAACCGT 742

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QY 737 TGTTCGCGCGGCATCATGAGCTCTGGAGCCATGCTGCGCTGTGACCCGGTGGACGGA 796
DB 743 TATTTTCGCGCTGGGATCATGCAAGTGTGCAATGTTACCCAGCGATGCGTTCGATGGA 802
QY 797 CGTAGGCAACAGATCTACGACCTCTTTGCTCGAGTGTGCTGCTGCGAGCGGCGG 856
DB 803 TCTATGGCAATGAGATCTTTGATCTGCTCGCTGCAATGCTGGTGGCTTTCGCGATCTG 862
QY 857 ACAAGCTCGCGTCTTGGCGAGTGGCTCTAGGCGACACCTTGTCTGATGCGACCAACA 916
DB 863 ATAAGTTGGCGCTTTCGGGAGTGTCAAGTGATACACTAGAGGATGCGACTAATATA 922
QY 917 CTCTCGGCTTCTGGGTAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 976
DB 923 CCCAGGCTTCTTAGCTTATAGCTTCCCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTG 982
QY 977 AGAATACACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1036
DB 983 TGAACATACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1042
QY 1037 TGATCATTTGGCGACACGAGGAGGACCATCTTTTGGGCTCTCTTTTGAACGTTGA 1096
DB 1043 TGAATTTGGAGACACGAGGAGGACCATCTTTTGGGCTCTCTTTTGAACGTTGA 1102
QY 1097 CCAAGATGCTCAGGCGCGCTTACTTCAAGAGTCTTTTCAAGAGTCTTTTCAAGAGTCT 1156
DB 1103 CCACGAGCGCAAGCTAGGAGTACTTTTAAAGAGAGTCTTTTCAAGAGTCTTTTCAAG 1162
QY 1157 AGATGACACCTTGTAGGCGGCTACCCAGGACATCACCAGGTTCTCGTTCGACA 1216
DB 1163 AGATTTGACATTAATGATGCTGCTACCCAGGAGTCTTTTCAAGAGTCTTTTCAAGAGT 1222
QY 1217 CGGCTGTTCTCAAGCGCTTCAACCGCGCTTCAAGAGTCTTTTCAAGAGTCTTTTCAAG 1276
DB 1223 CGGCGATCTTGAACTCTCAACCGCGCTTCAAGAGTCTTTTCAAGAGTCTTTTCAAG 1282
QY 1277 TTGCAATTCATCCGCGCGCTACTTCTCAACCGCTTCAAGAGTCTTTTCAAGAGTCT 1336
DB 1283 TTGCTTTCACTTAGCGCGCTTCAACCGCGCTTCAAGAGTCTTTTCAAGAGTCTTT 1342
QY 1337 GCTTCTCTTAAGAGCTCTTGGGTTGCCAATCATGGGACCTTCCATGCGCAACGACA 1396
DB 1343 CTTCCTGTCAAAGAGCTCAGTGGCTTGCCTGCTTGGTACATTCACAGCAACGACA 1402
QY 1397 TTGCTGGCAGGACTACTTGTGGAAAGCGGAGGCTCATCTCAACCAAGCGTTTATCG 1456
DB 1403 TCGTCTTCCAGAGCTACTTGTGCTCGGATCGGCTCTTATCTAATATATGCTTCTATG 1462
QY 1457 CGTTCCGACCGACTTGGACCCCAACAACGCGGCTTGTGGTGAATGCGCCCAAGTACA 1516
DB 1463 CTTTCGCTACGATCTTGATCAAAATACGCTGCTTCTTGTAAAGTGGCCAGAGTACA 1522
QY 1517 CCAGAGCTCTAGTCTGCAACACTTGTATGATGATCAACGCTTGGGCTGTACACCG 1576
DB 1523 CATCTTCTCAGTCTGGAATAATCTTATGATGATTAAGTCTTCTGCTTTTACACCG 1582
QY 1577 GCAAGCAAACTTCCGCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1636
DB 1583 GTAAGATAATTTTCAAGACAGCTGTTAGCTGCTCTTTCTTCTAATCCACCACTTTCT 1642
QY 1637 TTGT 1640
DB 1643 TCGT 1646

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RESULT 7

US-09-943-857-1
; Sequence 1, Application US/09943857
; Publication No. US20030124701A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Jei-Fu
; APPLICANT: Lee, Guan-Chiun
; APPLICANT: Tang, Shye-Jye

```

; TITLE OF INVENTION: RECOMBINANT CANDIDA RUGOSA LIPASES
; FILE REFERENCE: 08919-066001
; CURRENT APPLICATION NUMBER: US/09/943,857
; CURRENT FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1469
; TYPE: DNA
; ORGANISM: Candida rugosa
; US-09-943-857-1

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Query Match 47.4%; Score 778.4; DB 10; Length 1469;
Best Local Similarity 75.7%; Pred. No. 6e-210;
Matches 1200; Conservative 0; Mismatches 261; Indels 125; Gaps 14;

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QY 51 CAAGCTCCGCAACGGCGACACCATCACCGGTCTCAAGCCATCATCAAGAGCGGTTCCT 110
DB 8 CCACCTCGCCAAACGGCGACACCATCACCGGTCTCAAGCCATTTGTCAACGAAAGTTTCT 67
QY 111 CGGCATTCCCTTTTGGCGAGCGCGGTGGGCAACCTCGCTTCAAGGACCCCTGTGCGGTA 170
DB 68 CGGCATACCGTTTGGCGAGCGCGCGTGGCA--CTCGCTTCAA----- 110
QY 171 CTCTGGCTCGCTCAACGGCCAGAAAGTTTCACTTTTACGGCCCGCTTGTGATGACAGAA 230
DB 111 -----GCTCAACGGCCAGAGTTTAC-----CTACGCGCCGTGCATGACAGTAA 155
QY 231 CCCGAGGCGAGTTTGAAGAGAACCTTGGGCAAGCGGACTCGGACTTGGTGTGATGAGTTC 290
DB 156 CCTATGGGCTCGTTTCA----- 187
QY 291 CAAAGTGTTCAGAGCGGTGCTTCCCGAGTGAAGACTGCTTCAACCATCAAGTGGTGGC 350
DB 188 CAAAGTCTTCAAGTGTGCTTCCCGAGTGAAGACTGCTTCAAC----- 232
QY 351 CGCCCGGCGACCAAGCGCGCGCAACCTCCCGGTCTATGCTCTGGATCTTTGGCGGTGG 410
DB 233 -----CACCAGGCGCAGTGTGCTTCCCGGTGATGCTTGGATCTTTGGCGGTGG 283
QY 411 GTTTGAGATCGGCGAGCCCCACCATCTTCCCTCCCGCCAGATGCTCAAGAGTGTGCT 470
DB 284 GTTTGAGCTTGGCGGCTCCAGCTCTTTTCCAGGAGACCAAGATGCTGCGCAAGAGCGTCT 343
QY 471 CATGGCAAGCACATCATCACGCTGGCGTCACTACCGTGTGCTCTGCTGGGCTTCTT 530
DB 344 CATGGTAAACCGGTGATCCACGTAGCATGAACCTACCGGTGGCGTCTATGGGGTCTT 403
QY 531 GGCTGGTGAATGACATCAAGGCGGAGGCGGGAACCGCGGCTTTGAAGGACACAGCTTT 590
DB 404 GCGCGGCCCGGACATCCAGAACGAAGGACGCGGGAACGCGGCTTGCATGACACGCGCTT 463
QY 591 GGGCATGCGAGTGGGTGGCAGAACATTTGCGGGTTCCGGGCGGACCCGAGCAAGGTGAC 650
DB 464 GGGCATGCGAGTGGGTGGCAGAACATTTGCTGGGTTTGGCGGCGACCCGAGCAAGGTGAC 523
QY 651 TATCTTTGGCGAGTCTGGCGGACGATGCTCGTGTGTGCGCAACCTCATCTGCAAGCAGG 710
DB 524 CATATACGGCGAG---GCGGCGACATGTCGACGTTTGTGCACTTGTGTGAAACGAGCG 580
QY 711 CGACAACACGTACAAGGGCAAGCGGTTTTCGCGCGGGGACATCATGCAAGTCTGGAGCCAT 770
DB 581 CGACAACACGTACAAGCGGAGCGGTTTTCGCGCGCGCCATCATGCAAG-----GGCTG 634
QY 771 GGTGCGCTCTGACCCCGGTGGAGCGGACGTACGGCAACGAGATCTACGACCTCTTTGTCTC 830
DB 635 CATGGTGGCGGACCCCGGTGGAGCGGACGTACGGCAACGAGATCTACACAGGTGGTGGC 694
QY 831 GAGTGTGGCTGTGCGAGCGGACGAGCAAGCTCGCGTGTGCTGCGAGTGGTCTTAGCGA 890
DB 695 GTCTGCGGGGTGGCAGTGGCAGCAAGCTCGCGTGTGCGCGGCTTTTCTCAGGA 754
QY 891 CACCTTGTGATGCCAACCAACACACTCTCTGGGTCTTGTGGCGTACTCTCTGTTGCGGTT 950

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Db 755 CAGCTTGATACAGGCCACAGCGACACGCGCGCGGTGTTGGCGTACCCGTCGTTGGGTT 814
Qy 951 GTCTATATCTCCGCGGCCGACGCGCAAGAACATCAACCGATGATGTACAAAGTTGGTGG 1010
Db 815 G---TATCTCCGCGCGGCCGACGCGACCTTATCAACCGACGACATGTATGCCCTGGTGG 871
Qy 1011 CGACGGCAAGTATGAAGGTTCCGCTGATCTATTCGCGACGACGAGGAGGACCAT 1070
Db 872 GGACGGCAAGTATGACACAGTCCCGGTGATCTCGCGACCGACGAGGAGGACATTT 931
Qy 1071 CTTTGGGCTCTCTTTTGAACGTCACACGATGCTCAGGCCCGTGTCTACTTCAAGCA 1130
Db 932 GTTGGGCTC-----TTGAACGTGACACAGATGCTCAGGACCGGGGTACTTCAAGCA 985
Qy 1131 GTCTTTCAFCACGCGACGCGAGATCGACACTTTGATGCGGGGTACCCCGAGCA 1190
Db 986 G---TTCAATCCACGCGCAGCGATGCGAGATCGACAGCTTGTATGCGGGGTACACGAGCA 1042
Qy 1191 GATCACCCAGGTTCTCCGTTTCGACACAGGGTGTCTCAACGCCCTCACCCCGCAGTTCAA 1250
Db 1043 CATCACCCAGGG---TCCGTTTCGACACCGGCATCTTCAATGCGCATCACCCCGCAGTTCAA 1099
Qy 1251 GAGAACTCTCGCGTGTCTCGCGACCTTGCTCATTTCAATCCACGCGCCGCGTACTTCTCAA 1310
Db 1100 ACGGATC---GCGTTGCTTGGCGACCTTGGCTTCAAGCTTGGCGGTGCTACTTCTCNA 1156
Qy 1311 CCATTTCCAGGCGCGCACAAAGTACTCGTTCTCTCTAAGCAGCTCTCTGGGTGCCAAT 1370
Db 1157 CTACTACCAAGGCGCGCACAAAGTACTCGTTT-----TCAAAGCAGCTTGGGTGCCGCT 1209
Qy 1371 CATGGCAGCTTCCATGCGCAACGACATGTGTGCGCAGGACTACTTGTGGGAGCGGCGAG 1430
Db 1210 CTTGGGACCTTTCACGCGCAACGACATCTGCGAGGACTACTTGGTGGGAGCGGCGAG 1269
Qy 1431 CGTCTATACAAACACGCGTTTATCGCGTTCCGCCACCGACTTGGACCCCAACACCGCGGG 1490
Db 1270 TGTGATACACACGCGTTCTATTTGGTTTCGCCAAGCCTCGACCCCGACAAAGCGGG 1329
Qy 1491 GTTGTGGTGAATCGCGCCAAAGTACACGAGAGCTCTCAGTCTGGCAACAACTTGATGAT 1550
Db 1330 CTTGTGGACAACTGCGCCACCTACACGAGCAGC-----AGGGCAACAACTTGATGCA 1382
Qy 1551 GATCAACGCTTGGGCTGTACACCGCAAGCAACTTCCGACCGCTGGCTACGAGCG 1610
Db 1383 GATCAACGCTTGGGCTGTACACCGCAAGCAACTTCCGCGGATGCGGTACGCGC 1442
Qy 1611 GTTGATGACCAACCGCTCTTCTTTCT 1636
Db 1443 CCTCTTTTCCAAACCGCTTCTTTGT 1468

RESULT 8

US-10-369-493-27923
; Sequence 27923, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 27923
; LENGTH: 1687
; TYPE: DNA

i ORGANISM: Neurospora crassa
US-10-369-493-27923

Query Match 21.6%; Score 354.2; DB 17; Length 1687;
Best Local Similarity 55.7%; Pred. No. 9e-90;
Matches 811; Conservative 0; Mismatches 573; Indels 73; Gaps 4;

Qy 66 CGACACATACACCGGTCTCAAGCGCATCATCAACGAGCGGTTCCTCGGCATTCCTCTTGC 125
Db 27 CGGTACGATTTGGGTGCTTAACGGCATCTCTCACTGAGGCTTTCACACGGAATCCCTTAC 86
Qy 126 CGAGCGCGGTGGCAACCTCCGCTTCAAGAACCTCTGCGGTACTCTGGCTCGCTCAA 185
Db 87 CTTCTCTCGAGCGGCAACCTTGGCTCAAGCTCCCGTGAGACTTAAGTGTCTCTGGG 146
Qy 186 CGGCAGAAAGTTCACTTCTTACGCGCCGCTTGTGATGACGAGAACCCCGAGGGGACGTT 245
Db 147 TGTCTTTGATGCTCTGGCATCGGCCCTGCTTGGCCCCAGTTCTTGTGACACCTCGTC 206
Qy 246 TGAAGAGAACCTTGGCAAGACGCGACTCGACTTGGTGATGCGAGTCCAAAGGTGTTCCAGGC 305
Db 207 GAACGAGTTTCTGCCCTCA---GGTTATCGATAAGATCGTTAAACACGACGCTTTTCAAGAC 263
Qy 306 GGTGCTTCCCAGAGTGAAGACTGCTCTCACCATCAACGCTGTGTGCGCGCGCGGACCA 365
Db 264 TATACTCAAGCTCAAGGAGGACTGTTGACCATCTCGGTCACTGTCTCCAAAGGGACCA 323
Qy 366 GCGCGCGCCAACTCCCGGTCTGCTGTGATCTTGTGCGGTGGGTTTG----- 415
Db 324 GGTGTGATGAAGCTCCCGCTCTTTCTGGATCTTTGTGTGTTTCGAAGTGAGAAA 383
Qy 416 -----AGATCGCAGCCCCA 430
Db 384 TCCAGCTTATATACGCGATGTAATGAACAAAGTGTAAAACTTTCACAGCTCGAGTGGCGT 443
Qy 431 CCATCTTCCCTCCGCGCAGATGCTCAACAAAGAGTGTCTCATGGGCAAGCACATCATCC 490
Db 444 CCATGATCAGTGGCGCTCCCTAGTCAACCAAGCTATCAAATGGTAAAGCCGTACGTCT 503
Qy 491 ACGTGGCGCTCAACTACCGTGTGCTCTGCGGGGTCTTGGCTGGTGATGATCAAGG 550
Db 504 ACGTTGCGCTCAACTACCGTGTGCTGCGGTGCTTGGTTTCAATGCCCGGAAAGAGATCTTTA 563
Qy 551 CCGAGGCGAGCGGGAACCGCGCTTGAAGGACGAGCGTTTGGGATGACAGTGGGTGGGAG 610
Db 564 AGGACGCGCTCTTCAAACTTGGGTCACTTGACACGAGCATGGGCTTCCAGTGGGTGGCG 623
Qy 611 ACAACATTTGCGGGTTTCCGCGCGACCGACGAGCAAGGTGACTATCTTTGGCGAGTCTGGCG 670
Db 624 ACACATTTGCTGCTTCCGCGGTGACCCAGACAGGTCACTATCTGGGGCGAGTCCGCG 683
Qy 671 GAGCATGTCGTTGTGTCACCTCATCTCGAAACGACGCGGACAAACGCTACAGGGA 730
Db 684 GTGCCATGTCGCTTTTCAACACAGATGTCTCTATGACGGTGACAAACGCTACAAACGCA 743
Qy 731 AGCGGTTTTCGCGCGGCGCATCATGCACTCTGGAGCCATGGTGGCGTCTGACCCGCTGG 790
Db 744 AGCCCTTTTCCGTGGCGCCATCATGAATCTGGTTTCATCGTCCCCCGCGGCCCGCTCG 803
Qy 791 ACGCACGTACGCGAAACAGATCTACGACCTCTTTGTCTCGAGTGTGCTGGTGTGGCAGCG 850
Db 804 ACTGCCCAAGGCGCAAGAGTCTACGACACCGCTCAAGNACCGCGGCTGCTCTGGTG 863
Qy 851 CCAGGCAACAGCTCGCGTGTGGCGAGTGGCTTACGAGCACTTGTGATGACCA 910
Db 864 CTGTGACACACCTTGTGCTGCGCGCTCTTCCCTACGAGACTTTTCTCAAGGCGCGTA 923
Qy 911 ACACACTCTTGGGTTCTTGGGCTACTCTCTGTTGGGTGTTCTATCTCCGCGGCGCG 970
Db 924 ACTCGTGCCTGGGATCTCTGCTGAACAACTCGTTGCTCTTTCTTACCTCCGCGACCG 983
Qy 971 ACGGCAAGAACATCACCGATGACATGTACAAAGTTGGTGGCGGACGGCAAGTATGCAAGCG 1030

Db 984 ATGGCAAGGCTTGTGACTCAGAGCGCCGATTAAGCTCATGCTCGCTAAGAGTACGCGCGCG 1043
QY 1031 TTCCCGTGATCATTTGGCGACAGAACGACGAGGCGCACATCTTTGGGCTCTCTTCTTTGA 1090
Db 1044 TCCCCATGATCATCGGGGATCAAGAGGATGAGGGCACTCTCTTCTCCCTCTTCCAGGCA 1103
QY 1091 ACCTGACCAAGATGCTCAGCGCGGTCTTACTTCAAGCAG----TCTTTTCATCCAGGCA 1147
Db 1104 ACATCACCAACACAGCAAGCTGGTCAGCTTACCTCAACGATATCTTCTTCAACGAGGCA 1163
QY 1148 GCGACGCGGAGATCGACACCTTGTATGCGGCGGTACCCAGGACATCACCGGGTCTC 1207
Db 1164 CCGAGTTCGAGATTAAGTCTCTGCTCGTACCTTACAGTACCTTATCTCGCGGGTCTCG 1223
QY 1208 CGTTGACACGGGTGTTCTCAACGCGCTCACCCGCGAGTTCAAGAGAACTCTTCGCGGTG 1267
Db 1224 CTTTGGCACCGGCTCTTCAACGAGATTACCCCGGCTTCAAGCGCTTGGCGGCAATTC 1283
QY 1268 TCGGCACTTGCATTCATTCACGCGCGCGGTACTTCTCTCAAC-----CACT 1315
Db 1284 TTGGCGATCTCATCTTCAACCTCAGCGCGCGCATCTTCTCGACGCGCGCACCACTCTCA 1343
QY 1316 TCCAGGCGGCGACCAAGTACTGTTCTCTCTTAAGCAGCTCTTGGGTTGCCAATCATGG 1375
Db 1344 ACCCTCGGTGCGCGCTGGTGTATCTTGGCTTTACAACTTTGGCACACCCATCTTG 1403
QY 1376 GCACCTTCCATGCCAACGACATTTGTGTGGCAGGACTACTTGTGGGAAGCGGAGGTCA 1435
Db 1404 GAACCTTTACGCGCTCGGATATCTCGAGGTGTTCTACGGCATCTTGGCCAACTAGCGCA 1463
QY 1436 TCTAACAAACGGGTTT 1452
Db 1464 GCAAAAGCATCCAGTCT 1480

RESULT 9

US-09-801-852A-1
; Sequence 1, Application US/09801852A
; Patent No. US20020048781A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Chiang, Shu-Jen
; APPLICANT: Jonathan, Basch
; TITLE OF INVENTION: DIRECT PRODUCTION OF DESACETYLCEPHALOSPORIN C
; FILE REFERENCE: ON0163
; CURRENT APPLICATION NUMBER: US/09/801,852A
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/188,033
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1716
; TYPE: DNA
; ORGANISM: Rhodospiridium toruloides
US-09-801-852A-1

Query Match 7.3%; Score 119.6; DB 9; Length 1716;
Best Local Similarity 53.8%; Pred. No. 2.6e-23;
Matches 301; Conservative 0; Mismatches 244; Indels 15; Gaps 2;
QY 322 GAGGACTGCTTACCATCAACGTGTGCGCGCGCGGACCAAGCGGGCGGCCAACCTC 381
Db 361 GAGGATTGCTCTTCTCTCAATGTCGTTGCCCCCGCGGCTCTGCGAGGGCGACATCTT 420
QY 382 CCGGTATGCTCTGATCTTTGGCGGTGGTTTGTAGATCGGACGCCCAACCATCTTCCCT 441
Db 421 CCGGCTCTGCTACATTCACGAGGTGGCTACGCGCTTCGGGATGCGAGCACCGGCAGC 480
QY 442 CCGCGCCAGATGTCACCAAGAGTGTGCTCATGGGCAACACATCATCCAGCTGGCGCTC 501
Db 481 GACTTTGCGCGCTTACCAA-----GCACGCGGAACCAAGATGGTGTGTTAAATCTC 534

QY 502 AACTACCGTGTGCTCTGTTGGGTTCTTTGGCTGTGTGATCATCAAGGCCGAGGCGCAGC 561
Db 535 CAGTACCGTCTCGGAGCTTTGGTTTCTCGCTGGCCAAAGCCATGAAGGACTACGGTGTGA 594
QY 562 GGGAAAGCCCGGCTTGAAGGACAGCGTTTGGGATGTCAGTGGGTGGCAGACAACATTTGCC 621
Db 595 ACGAAGCCCGGCTTGTGACCAAGAAATTCGCGCTTCAATGGGTTTCAACAGCACGCTCTCG 654
QY 622 GGGTTGGGCGGACCCGAGCAAGGTGACTATCTTTGGCGAGTCTGCGGGGAGCATGTCTC 681
Db 655 AAGTTTCGGCGGCAACCCCGATCAGTTAGATTTGGGGCGAGTCTCGAGCGGAGGTTCC 714
QY 682 GTTGTGTGCACCTCATCTGGAACGACGCGGCAACAACGTAACAAGGC-----AAG 732
Db 715 GTTATGAACACGATCATTCGGAACGCGCGCAACACCGTCAAGGCTCTCGTCTCAAGAAG 774
QY 733 CGGTGTTTCGGCGGCGGATCATGAGTCTTGAGGCAATGGTGGCGTCTCACCGGTGGAC 792
Db 775 CCGCTCTTTCACGCTGCCATCGGCTCTCCGTTCTCTCCCTACCAAGCCAAGTACAAC 834
QY 793 GGCACGTAGCGCAACGAGATCTACGACCTCTTTGTCTCGAGTGTGCTGTGGCAGCGCC 852
Db 835 TCCCCTTCGCGAGGCTGCTCTACTCCCAACTCGTCTCGGCGACAACCTGCACCAAGGCC 894
QY 853 AGCGACAAGCTCGCGTGTCTT 872
Db 895 GCCTCGTCTCTCGCTTGGCT 914

RESULT 10

US-10-369-493-41665
; Sequence 41665, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 41665
; LENGTH: 1272
; TYPE: DNA
; ORGANISM: SPHINGOMONAS
US-10-369-493-41665

Query Match 6.3%; Score 103.8; DB 17; Length 1272;
Best Local Similarity 53.4%; Pred. No. 7.1e-19;
Matches 241; Conservative 0; Mismatches 207; Indels 3; Gaps 1;
QY 322 GAGGACTGCTTACCATCAACGTGTGCGCGCGCGGACCAAGCGGGCGGCCAACCTC 381
Db 223 GAGGACTGCTTGTATCTCAACGTGTGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCTG 282
QY 382 CCGGTATGCTCTGATCTTTGGCGGTGGTTTGTAGATCGGCGAG--CCCAACCATCTTC 438
Db 283 CCGGTATGCTTGTAGATCTAGCGCGCGGATTCGTGAACCGCGGTGCTCTCCCCCACC 342
QY 439 CTTCCCGCCAGATGTCACCAAGAGTGTGCTCATGGGCAAGCAATCATCCAGCTGGCC 498
Db 343 TATGCGGCAACAACCTGGCGAAGCAGGCGGTGCTGTTGTCAGCTTCAACTACCGGTC 402
QY 499 GTCAACTACCGTGTGCTCTGCGGGTCTTGGCTGTGTATGATCATCAAGCCAGGCGC 558
Db 403 GGCGCTTTCGCGAGCTTCGCCCTTCGCCCAACTCAGCCGCGAAGACGCGGATGGCGGGCTG 462

QY 890 ACACCTTGTCTGATGCCAACAAACACTCTCTGGGTTCTTGGGTAATACTCTCTGTTCCGGT 949
Db 923 CAGCGCAGGTCTCTGTGTGAACACCAAGATGGCACGTGCTGTCTCAAGAAAGCGTCTTCCGGT 982
QY 950 TGTCTTATCTCCCGCGCCGCGGAGGAGCAAGAACATACCGATGACATGTAAGATTGGTGC 1009
Db 983 TCTCTTCTGTCTGTGTGTAGATGGAGACTTCTCTAGTGAACCCAGAGGCCCTCATCA 1042
QY 1010 GCGACGGCAAGTATGCAAGCGTTTCCCGTGATCATTTGGCGACACGACGAGGGCACCA 1069
Db 1043 ACGCGGAGACTTCCACGGCTGTCAGTGTCTGTGGTGTGGTGAAGATGAGGGCTCT 1102
QY 1070 TCTTTGGGCTCT 1081
Db 1103 ATTTTCTGGTTT 1114

RESULT 13

US-10-792-491-5
; Sequence 5, Application US/10792491
; Publication No. US20040148657A1
; GENERAL INFORMATION:
; APPLICANT: Mor, Tsafir S.
; APPLICANT: Soreq, Hermona
; APPLICANT: Arntzen, Charles J.
; APPLICANT: Mason, Hugh S.
; TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HUMAN ACETYLCHOLINESTERASE IN
; TITLE OF INVENTION: TRANSGENIC PLANTS
; FILE REFERENCE: BTI-45
; CURRENT APPLICATION NUMBER: US/10/792,491
; CURRENT FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: 60/190,440
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent In Ver. 3.1
; SEQ ID NO 5
; LENGTH: 1725
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: human acetylcholinesterase gene optimized for
; OTHER INFORMATION: expression in plants
US-10-792-491-5

Query Match 4.5%; Score 74.4; DB 22; Length 1725;
Best Local Similarity 47.1%; Pred. No. 1.6e-10;
Matches 373; Conservative 0; Mismatches 401; Indels 18; Gaps 4;
QY 290 CCAAGGTGTTCCAGGCGGTGCTTCCCGAGAGTGAGGACTGCTCACCATCAACGTGGTGC 349
Db 341 CCGAGATGTGGAACCCCAACCGTGAGCTGAGCGAGGAGTCTGTACCTCAAC---GTGT 397
QY 350 GCGCGCGGGGACCAAGCGGGGGCGCAACTCCCGGTATGCTCTGGATCTTTGGCGGTG 409
Db 398 GGACACCATACCCCGGCTATACATCCCAACCCCTGCTCTCTGGATCTATGGGGGTG 457
QY 410 GGTGTTGAGTCCGAGCGCCACCATCTCCCTCCCGCCAGATGTCACCAAGATGTGC 469
Db 458 GTTCTTACAGTGGGGCTCTCTTTGGAGCTGTACGATGGCCGCTTC-----TTGG 508
QY 470 TCATGGGCAAGCACATCATCCACGTGGCGGTCAACTACCGTGTGTGCTCTGTGGGGGTCT 529
Db 509 TACAGGCCGAGAGGACTGTGTGTGTCTCATGAACTACCGGTGGGAGCTTTGGCTTCC 568
QY 530 TGGCTGTGTATGACATCAAGCGCGGAGGAGCGGAAACCGCGCTTGAAGGACCAAGCTT 589
Db 569 TGGCCCTGCGGGGAGC---CGAGAGGCCCGGGCAATGTGGTCTCTCTGGATCAGAGGC 625
QY 590 TGGGATCAGTGGGTGGCAGACATCTCCGGGTTCGGCGGCGACCGGACCAAGGTGA 649
Db 626 TGGCCCTGAGTGGGTGACGAGAAACGTGGCAGCTTGGGGGTGACCCGACATCAGTGA 685

QY 650 CTATCTTTGGCGAGTCTGCGGCGAGCATGTCCGTGTGTGTCACCTCATCTCTGAAACGAG 709
Db 686 CGCTGTTTGGGAGAGCGCGGGAGCCGCTCGTGGGATGCACCTGTCTGCCCGCCCA 745
QY 710 GGCACAAACAGTATCAAGGGCAAGCCGTGTGTTCCGCGCGGGCATCATGCAAGTCTGGAGCCA 769
Db 746 GCGCGGGCGTGTTCACACAGGGCGGTGCTGCAAGAGCGGTGCCCCCAATGGAACCTTGGGCCA 805
QY 770 TGGTCCCGTCTGACCCCGTGGACGCGCATGCGCAACGAGATCTACGACCTCTTTGTCT 829
Db 806 CGGTGGGATGAGGAGAGGCCCTGTCAGG---GCCACGAGCTGGCCCACTCTGTGGGT 862
QY 830 CGAGTGTGGTGTGGCAGCGCCAGCAAGCTCCGCTGTGTCGCGAGTGCCTCTAGCG 889
Db 863 GTCTCCAGGCGGCACTGTGGGAATGACACAGAGCTGGTAGCTGCTTCCGACACGAC 922
QY 890 ACACCTTGTCTGATGCCAACCAACACTCTCTGGGTTCTTGGCGTACTCTCTGTGGCGT 949
Db 923 CAGCGCAGGTCTCTGTGAAACCAAGATGGCAGCTGCTCTCAAGAAAGCGTCTTCCGCT 982
QY 950 TGTCTTATCTCCCGCGGCGCGGCAAGAACATCAACGATGACATGTACAAAGTTGGTGC 1009
Db 983 TCTCTTCTGTGCTGTGTAGATGGAGACTTCTCTAGTGAACACCCAGAGGCCCTCATCA 1042
QY 1010 GCGACGGCAAGTATGCAAGCGTTTCCCGTGATCATTTGGCGACACGAAACGAGGGCACCA 1069
Db 1043 ACGCGGAGACTTCCACGGCTGACAGTGTCTGGTGGTGTGGTGAAGATGAGGGCTCT 1102
QY 1070 TCTTTGGGCTCT 1081
Db 1103 ATTTTCTGGTTT 1114

RESULT 14

US-10-887-553A-108
; Sequence 108, Application US/10887553A
; Publication No. US20050085436A1
; GENERAL INFORMATION:
; APPLICANT: Garza, Dan
; APPLICANT: Li, Hao
; TITLE OF INVENTION: Method to treat conditions associated
; TITLE OF INVENTION: with insulin signalling dysregulation
; FILE REFERENCE: 4-33262
; CURRENT APPLICATION NUMBER: US/10/887,553A
; CURRENT FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: 60/485,883
; PRIOR FILING DATE: 2003-08-07
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108
; LENGTH: 2909
; TYPE: DNA
; ORGANISM: human
US-10-887-553A-108

Query Match 4.5%; Score 74.4; DB 21; Length 2909;
Best Local Similarity 47.1%; Pred. No. 1.9e-10;
Matches 373; Conservative 0; Mismatches 401; Indels 18; Gaps 4;
QY 290 CCAAGGTGTTCCAGGCGGTGCTTCCCGAGAGTGAGGACTGCTCACCATCAACGTGGTGC 349
Db 435 CCGAGATGTGGAACCCCAACCGTGAGCTGAGCGAGGACTGCTGTACCTCAAC---GTGT 491
QY 350 GCGCGCGGGGACCAAGCGGGCGGCAACCTCCCGGTATGCTCTGGATCTTTGGCGGTG 409
Db 492 GGACACCATATCCCGCGGCTATACATCCCAACCCCTGCTCTCTGGATCTATGGGGGTG 551
QY 410 GGTGTTGAGTCCGAGCGCCACCATCTTCCCTCCCGCCAGATGTCACCAAGATGTGC 469
Db 552 GTTCTACAGTGGGGCTCTCTCTTGGAGCTGTAGATGGCGGCTTC-----TTGG 602
QY 470 TCATGGGCAAGCACATCATCAACGCTGGCGGTCAACTACCGTGTGCTCTGCGGGGTCT 529

Db 603 TACAGCCGAGAGGACTGTGTGTCATGAATACCGGGTGGAGCCTTTGGCTTCC 662
 Qy 530 TGGCTGGTATGATCAAGCCAGGCGGGAACCGCGCTTGAAGGACACAGCGTT 589
 Db 663 TGGCCCTGCGGGGAGC---CGAGAGGCCCGGGCAATGTGGGTCTCTCTGGATCAGAGC 719
 Qy 590 TGGGCATGAGTGGGTGGCAGACAACATTTGCCGGGTTCCGGCGGCGACCCGAGCAAGGTGA 649
 Db 720 TGGCCCTGAGTGGGTGGCAGAGAACGTGGAGCCCTTCGGGGGTGACCCGACATCAGTGA 779
 Qy 650 CTATCTTTGGGAGTCTGCGGGCAGCATGTCCGTGTGTGTCACCTCATCTGGAACGAGC 709
 Db 780 CGCTGTTTGGGAGAGCGCGGAGCGCCTCGGTGGGCATGCACCTGTCTGTCCCGCCCA 839
 Qy 710 GCGACAACAGTACAGGGCAAGCCGTTGTTCCGGCGGGGCATCATGAGTCTGGAGCCA 769
 Db 840 GCGGGGCGCTGTTCCAAGGGCGGTGTCTGAGAGCGGTGCCCCCAATGGACCCCTGGGCCA 899
 Qy 770 TGGTGGCGTCTGACCGGTTGGACGCGCATGTCAGGCAACGAGATCTACGACCTCTTTGTCT 829
 Db 900 CGGTGGGCATGGAGAGGCCCTCGCAGG---GCCACGAGCTGGCCCACTTTGGGCT 956
 Qy 830 CGAGTCTGGCTGTGGCAGCGCCAGCAAGCTCGCGTGTGGCGAGTGGCTCTAGCG 889
 Db 957 GTCTCCAGCGGCACTGGTGGGAATGACACAGAGCTGGTAGCTGCCCTTCGAGACAGAC 1016
 Qy 890 ACACCTTGTCTGATGCCACAACACACTCTCTGGGTTCTGGGCTACTCTCTGGTGGCT 949
 Db 1017 CAGCGCAGGTCTCTGTGGTGAACCAAGATGGCAGCTGTCTCAAGAAAGCGTCTTCGCGT 1076
 Qy 950 TGTCTTATCTCCCGCGCCGCGGCAAGAACATCACCGATGACATGTAACAAGTTGGTGC 1009
 Db 1077 TCTCTCTGCTGTGGTAGATGAGACTTCTCAGTGACACCCAGAGGCCCTCATCA 1136
 Qy 1010 GCGACGGCAAGTATCAAGCTTCCCGTGTATGTCGACCAAGTGGCGACCAAGCGAGGGCACCA 1069
 Db 1137 ACGCGGAGACTTCCACGCGCTGCAGGTCTGTGGGTGTGGTGAAGGATGAGGCTCGT 1196
 Qy 1070 TCTTTGGGCTCT 1081
 Db 1197 ATTTCTGGTTT 1208

RESULT 15
 US-09-810-861B-3
 ; Sequence 3, Application US/09810861B
 ; Patent No. US20020162140A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mor, Tsafir S.
 ; APPLICANT: Soreq, Hermona
 ; APPLICANT: Arntzen, Charles J.
 ; APPLICANT: Mason, Hugh S.
 ; TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HUMAN ACETYLCHOLINESTERASE IN
 ; FILE REFERENCE: BTI-45
 ; CURRENT APPLICATION NUMBER: US/09/810,861B
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR FILING DATE: 2000-03-17
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn Ver. 3.1
 ; SEQ ID NO 3
 ; LENGTH: 5767
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: plasmid vector
 ; OTHER INFORMATION: pTW034.
 US-09-810-861B-3

Query Match 4.5%; Score 74.4; DB 9; Length 5767;
 Best Local Similarity 47.1%; Pred. No. 2.2e-10;
 Matches 373; Conservative 0; Mismatches 401; Indels 18; Gaps 4;

Qy 290 CCAAGGTGTTCCAGCGGTGCTTCCCGAGAGTGAAGACTGCCTCACCATCAACGTGGTGC 349
 Db 1178 CCGAGATGTGGAACCCCAACCGTGAAGTGAAGAGGACTGCCTGTACCTCAAC---GTGT 1234
 Qy 350 GSCCGCCGGGACCAAGGCGGCGCAACCTCCCGGTTCATGCTCTGGATCTTTGGCGGTG 409
 Db 1235 GGAACACATACCCCGGCTTACATCCCAACCCCTGTCTCTGTCTGGATCTATGGGGTG 1294
 Qy 410 GGTTTGAGATCGGCAAGCCCAACATCTTCTCCCGCCAGATGTCTACCAAGAGTGTGC 469
 Db 1295 GCTTCTACAGTGGGGCTCTCTCTTGGACGTGTACGATGGCGGCTTC-----TTGG 1345
 Qy 470 TCATGGGCAAGCAGATCATCCAGCTGGGCGGTCAATACGCTGTTCCTGTGGGGGTCT 529
 Db 1346 TACAGGCGAGAGGACTGTGTGTGTCTTCAATCAATACCGGTGGGAGCTTTGGCTTCC 1405
 Qy 530 TGGCTGGTGTGATGACATCAAGGCGGAGGAGCGCGGAAACCGCGGCTTGAAGGACACAGCGTT 589
 Db 1406 TGGCCCTGCGGGGAGC---CGAGAGGCCCGGGCAATGTGGGTCTCTGTGATCAGAGC 1462
 Qy 590 TGGGCATCAGTGGGTGGCAGACAATTTGCCGGGTTCGGCGGCGACCCGAGCAAGGTGA 649
 Db 1463 TGGCCCTGAGTGGGTGACAGGAGAACGTGGCAGCCTTCGGGGGTGACCCGACATCAGTGA 1522
 Qy 650 CTATCTTTGGCGAGTCTCGGGCAGCATGTCCGTGTGTGGCCACCTCATCTGGAACGAGC 709
 Db 1523 CGCTGTTTGGGAGAGCGCGGAGCGCCCTCGGTGGGCAATGCACCTGTCTGCCGCCCA 1582
 Qy 710 GCGACAACAGTACAAAGGCGGCAAGCGTTGTTCCGGCGGCGCATCATGAGTCTGGAGCCA 769
 Db 1583 GCGGGGCTGTTTCAAGAGGCGGTGTGACAGGCGGTGCCCCCAATGGACCTGGGCA 1642
 Qy 770 TGGTGGCTGTGACCCCGGTGACCGCATGACGCAACGAGATCTACGACCTCTTTGTCT 829
 Db 1643 CGGTGGCATGGAGAGGCCCGTGCAGG---GCCACGAGCTGGCCCACTTTGGGCT 1699
 Qy 830 CGAGTGTGGCTGTGGCAGCGCCAGCAGCATGCTGGTGGGATGACACAGAGCTGGTACCTCGGACACGAC 889
 Db 1700 GTCTCCAGGCGGCACTGGTGGGATGACACAGAGCTGGTACCTCGGACACGAC 1759
 Qy 890 ACACCTTCTCGATGCCACCAACACTCTCTGGGTTCTTGGCGTACTCTCTGTTGCGGT 949
 Db 1760 CAGCGCAGGTCTGTGTGAACCAACGATGGCAGCTGTGCTTCAAGAAAGCTCTTCGGT 1819
 Qy 950 TGTCTTATCTCCCGGCGCCGACGCAAGAACATCACCGATGACATGTAAGTTGGTGC 1009
 Db 1820 TCTCTTCTGCTGTGTGTAGATGAGACTTCTCAGTGACACCCAGAGGCCCTCATCA 1879
 Qy 1010 GCGAGCGCAAGTATGCAAGCGTTCCCGTGTATCATTTGGCGCATGAGAGGGGACCA 1069
 Db 1880 ACGCGGAGACTTCCACGCGCTGCAGGTGTGTGGGTGTGGTGAAGGATGAGGGCTCGT 1939
 Qy 1070 TCTTTGGGCTCT 1081
 Db 1940 ATTTCTGGTTT 1951

Search completed: September 22, 2005, 10:32:41
 Job time : 1750 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 17, 2005, 07:32:23 ; Search time 43 Seconds
(without alignments)
949.606 Million cell updates/sec

Title: US-09-943-857A-4
Perfect score: 2864
Sequence: 1 SMNSKGPAGRLGVSPTAKLA.....DNFRTAGYDALMTNPSSFFV 547

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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2: /cgn2_6/ptodata/1/1aa/5B-COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A-COMB.pep.*
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5: /cgn2_6/ptodata/1/1aa/PTUS-COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1107	38.7	563	3	US-08-362-525-12 Sequence 12, Appl
2	672.5	23.5	574	4	US-10-023-515-4 Sequence 4, Appl
3	491.5	17.2	575	1	US-08-348-920-1 Sequence 1, Appl
4	488.5	17.1	575	1	US-08-348-920-1 Sequence 2, Appl
5	454	15.9	614	3	US-08-446-100-25 Sequence 25, Appl
6	452	15.8	600	2	US-08-370-156-4 Sequence 4, Appl
7	452	15.8	600	3	US-08-814-095-4 Sequence 4, Appl
8	452	15.8	600	3	US-08-975-084-1 Sequence 1, Appl
9	452	15.8	602	6	5215909-11 Patent No. 5215909
10	452	15.8	614	1	US-07-732-962A-2 Sequence 2, Appl
11	452	15.8	614	2	US-08-370-156-2 Sequence 2, Appl
12	452	15.8	614	3	US-08-446-100-19 Sequence 19, Appl
13	452	15.8	614	3	US-08-446-100-21 Sequence 21, Appl
14	452	15.8	614	3	US-08-814-095-2 Sequence 2, Appl
15	452	15.8	614	5	PT-US92-06106-2 Sequence 2, Appl
16	452	15.8	617	2	US-08-370-156-6 Sequence 6, Appl
17	452	15.8	617	3	US-08-814-095-6 Sequence 6, Appl
18	452	15.8	617	3	US-08-814-095-6 Sequence 6, Appl
19	452	15.8	645	4	US-09-949-016-7063 Sequence 7063, Ap
20	452	15.8	645	4	US-09-949-016-7064 Sequence 7064, Ap
21	451	15.7	602	3	US-08-446-100-1 Sequence 1, Appl
22	451	15.7	602	3	US-08-446-100-24 Sequence 24, Appl
23	451	15.7	602	3	US-09-334-489-3 Sequence 3, Appl
24	451	15.7	602	3	US-09-334-489-4 Sequence 4, Appl
25	451	15.7	643	4	US-09-949-016-11146 Sequence 11146, A
26	449.5	15.7	572	2	US-08-932-376A-2 Sequence 2, Appl
27	449	15.7	602	3	US-08-446-100-13 Sequence 13, Appl

28	448	15.6	602	3	US-08-446-100-11 Sequence 11, Appl
29	447	15.6	602	3	US-08-446-100-3 Sequence 3, Appl
30	447	15.6	602	3	US-08-446-100-4 Sequence 4, Appl
31	447	15.6	602	3	US-08-446-100-5 Sequence 5, Appl
32	447	15.6	602	3	US-08-446-100-12 Sequence 12, Appl
33	447	15.6	602	3	US-08-446-100-15 Sequence 15, Appl
34	447	15.6	602	3	US-08-446-100-16 Sequence 16, Appl
35	447	15.6	602	3	US-08-446-100-17 Sequence 17, Appl
36	447	15.6	602	3	US-08-446-100-18 Sequence 18, Appl
37	447	15.6	614	3	US-08-446-100-22 Sequence 22, Appl
38	447	15.6	614	3	US-08-446-100-23 Sequence 23, Appl
39	446	15.6	602	3	US-08-446-100-8 Sequence 8, Appl
40	445	15.5	602	3	US-08-446-100-14 Sequence 14, Appl
41	444.5	15.5	544	2	US-08-932-376A-4 Sequence 4, Appl
42	444.5	15.5	635	6	5215909-10 Patent No. 5215909
43	444.5	15.5	635	6	5215909-10 Patent No. 5215909
44	444	15.5	614	3	US-08-446-100-20 Sequence 20, Appl
45	443	15.5	573	6	5215909-12 Patent No. 5215909

ALIGNMENTS

RESULT 1
US-08-362-525-12
; Sequence 12, Application US/08362525
; Patent No. 6027910
; GENERAL INFORMATION:
; APPLICANT: KLIS, FRANCISCUS M.
; APPLICANT: SCHREUDER, MAARTEN P.
; APPLICANT: TOSCHKA, HOLSER Y.
; APPLICANT: VERRIPS, CORNELIS T.
; TITLE OF INVENTION: PROCESS FOR IMMOBILIZING ENZYMES TO THE
; TITLE OF INVENTION: CELL WALL OF A MICROBIAL CELL BY PRODUCING A FUSION
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/362,525
; FILING DATE: 04-JAN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 92202080.5
; FILING DATE: 08-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 92203899.7
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/01763
; FILING DATE: 07-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 213289/T7020(V)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 563 amino acids
; TYPE: amino acid

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-362-525-12

Query Match      38.7%; Score 1107; DB 3; Length 563;
Best Local Similarity 43.4%; Pred. No. 6.8e-100;
Matches 240; Conservative 73; Mismatches 196; Indels 44; Gaps 9;

QY 9  GRLGSVPTAKLANGDTITGLNAINIEAFGIIPAEPPVGNLRFKDPVPVSGSLNGQKFTS 68
Db 16  GTLAQAPTAVLANGNEVISGLGKVDVTFKGIIPADPPVGDLPFRKPPQPTGSGYQGLKAND 75
QY 69  YGPPSCMOQNEPCTFE-----ENLKGTAIDLVMQSKVQAVLPQSEDCLTINV 115
Db 76  FSSACMLDPGNFSLDKVGLKLPNLRGLYDMA-----QGSVMNEDCLYNV 129
QY 116  VRPPGKTAGANLPLMWIFGGFEGISPTIFFPAQMVTKSVLMGKHIIHVAHYRVASWG 175
Db 130  PRPAGTKPDALPLVMWIIYGGAFVFGSSASYFGNGYVKESVEMGQPVVVFVSINRTGPVG 189
QY 176  FLAGDDIKAGSGNAGLKQRLGMQWADNIAGFGDPSKVTIFGESAGSMSVLCHLIWN 235
Db 190  FLGGDAITAEGNTNAGLHQRLGLEWSDNIANFGGDPDKVMIFGESAGAMVAHQLVAY 249
QY 236  DGDNTYKGPLFRAGIMQSGAMVPSPDVPDGTGNEIYDLFVSSAGC---GSASDCLKACL 292
Db 250  GGDNTYNGQLFASAILQSGGLPYDPDSTSVGPESAYSRAQYAGCDTSASNDITLACL 309
QY 293  SASSDTLLDATNN-----TPGFLAYSSRLSLYLPDPDGKNITDDMYKLVRDQKYAS 343
Db 310  SKSSDVLHSAQNSYDLKDLFPQLGFG-----PRPDGNIIPDAAYELYRSGRYAK 362
QY 344  VPVIIGDQNDGTTIFGLSLNVTWNAQARAYKQSFIFHASDAEITLMAAYPQDITQSP 403
Db 363  VPIYITGNQDEGTTILAPVAINATTTTPHVKKWLKYICQASDASLDRVLSLYPGSWSEGP 422
QY 404  FDTGVNALTPOFKRISAVLGDIAFHARRYFLNHFQGGTKYSFLSKOLSGL-PIMGTFH 462
Db 423  FRIGILNALTPOFKRIAIIFTDLQLFQSPRVMLNATKQVNRWYIATQLHNLVPLGTFH 482
QY 463  ANDIVMQDYL-LGSGSVIYNNAFIATPDLDPNTAGLLVNNWPKYTSSQSGNNLMINAL 521
Db 483  GSDLLFQYVYDLGPSSA-YRRYFISFANHDDPNVGNLQQWDWYT---DAGKEMLIQIHI 538
QY 522  GLYTGKDNPRTAG 534
Db 539  GNSMRTDPRFIEG 551

RESULT 2
US-10-023-515-4
; Sequence 4, Application US/10023515
; Patent No. 6664091
; GENERAL INFORMATION:
; APPLICANT: Curtiss, Rory A. J.
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE
; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
; FILE REFERENCE: 10448-122001
; CURRENT APPLICATION NUMBER: US/10/023,515
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 60/256,369
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/279,508
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence

US-10-023-515-4
Query Match      23.5%; Score 672.5; DB 4; Length 574;
Best Local Similarity 34.9%; Pred. No. 4.4e-57;
Matches 195; Conservative 76; Mismatches 195; Indels 93; Gaps 18;

QY 35  AFLGIPPAEPVGNLRFKDPVPY----SGSLNGQKFTSYGPPSCMOQNEPCTFEENLGKTA 90
Db 19  SFLGIPYAEPPVGNLRFKAPQYKEPWSVDVDA---TKYPPSCLQDDDFGFSLSL-KVA 74
QY 91  LDVLMQSKVFOAVLPQSEDCLTINVVRPPGKTAGANLFLVLMWIFGGFEGISPTIFFPQA 150
Db 75  LKMLSLGNLKLVLKLSLCLVLYVTPKNTKPNKSLPVMWIIHGGMFGSGHSLPLSL 134
QY 151  MYTKSVLMGKHIIHVAHYRVASWGFLAGDDIKABGSGNAGLKQRLGMQWADNIAGFG 210
Db 135  YDGESLAREGNVIVVSYNIRLGLPLGFLSTGDDKLPFGSGNYGLLDQRLALKWYQDNIAAF 194
QY 211  GDPSKVTIFGESAGSMSVLCHLIWNDGNTYKGPLFRAGIMQSGA----MVPSPDPVDG 265
Db 195  GDNPSVTIFGESAGHASVSLLLLSNGGNDPPSSKGLFHRAISQSGALSPPWAIQSESNA 254
QY 266  TYGNEIYDLFVSSAGC---SASDCLKACLRSASDITLLDATNNTPGLAYS-----SLRLS 318
Db 255  GRAKELARLL---GCNETSSSELDDCLRSKSAELLEATRS---FLLPEYVPLPLFLA 307
QY 319  YLPRPDGKN-----ITDDMYKLVRDQKYASVPVIIGDQNDGTTIFGLSLNVTWNAQAR- 372
Db 308  FGPVVDGDDAPEAFIPEDPEBELIKEGKPADVPYLGIVTKDEGGYFAAMLLNASSKGEDEL 367
QY 373  -----AVFKQSPFHASDA-----EIDFLMAAYPQDITQSGPFDITGVNALTTP 414
Db 368  KKETNPVWLELLKYLIFYASEALNIKMDLLADLVLEKYPGDVDDFS-----VES 418
QY 415  QFKRISAVLGLAF-----THARR-----YFLNHFQGGTKYSFLSKOLSGLPTIM 458
Db 419  RKNPLQDMLTDLFLKCPTRVAADLHAKHGSPVYAVYVDHPASFGIGQFLAKRVDP-BFG 477
QY 459  GTFHANDI--VWQDYLL-----GSGSVIYNNAFIATPDLDPN--TAGLLVNW 502
Db 478  GAVHGEITFFVFGNPLKELQYKATEEBEESKSSKTMNYWANFAKTGNPNNGTSLVVM 537
QY 503  PKYTSSQSGNNLMINAL 521
Db 538  PKYTSEEKYSLLILLITTI 556

RESULT 3
US-08-348-920-1
; Sequence 1, Application US/08348920
; Patent No. 5695750
; GENERAL INFORMATION:
; APPLICANT: Doctor, Bhupendra P.
; APPLICANT: Maxwell, Donald
; APPLICANT: Saxena, Ashima
; APPLICANT: Radic, Zoran
; APPLICANT: Taylor, Palmer
; TITLE OF INVENTION: Compositions for Use to Deactivate
; TITLE OF INVENTION: Organophosphates
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John F. Moran
; STREET: Off. of Command Judge Adv., HQ USAMRDC, Fort
; STREET: Detrick
; CITY: Frederick
; STATE: MD
; COUNTRY: US
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/348,920
; FILING DATE: 25-NOV-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: doc348,920
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-7807
; TELEFAX: 301-619-7714
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 575 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; US-08-348-920-1

Query Match 17.2%; Score 491.5; DB 1; Length 575;
Best Local Similarity 30.4%; Pred. No. 2.9e-39;
Matches 164; Conservative 75; Mismatches 195; Indels 105; Gaps 24;

QY 22 GDTITGLNAINAEFLGIPFAEPVGNLRFKDP---VPYSGSLNGQKFTSYGSPSCMQNP 78
Db 17 GTRVPVLSHSIS-AFLGIPFAEPVGNMFRPEPKPWSGVWNASTY----PNNCQQV 71

QY 79 EGTFEENLGTALDLVMSQKVFQAVLPQSEDCLTINV-----VRPPTKAGANLPVLMWIF 134
Db 72 DEQFPFGSG-----SEMNPNNREMSDCLYLNIVPSPRKST-----TWVVIY 116

QY 135 GGGFEIGSPTIPPPAQWTKSVLMGKH-----IIHVAANYRVASWGFLA--GDDIKAG 186
Db 117 GGGFYSGSSTL-----DVYNGKYLAYTEEVVLVSLSYRVGAFGLALHGSQ---EA 164

QY 187 SGNAGLKDOORLGMQWADNIAGFGDPKSVTIIFGSAGSMVLCILWINDGNTYKGPL 246
Db 165 PGNVGLLDORLQWALQVHDNIQFFGDPKVTIIFGSAGSAGVGMHIL-----SPGSRDL 218

QY 247 FRAGIMQSGAMVPSDP---VDGTYGNEIYDLFVSSAGCGSASDK--LACLRASASDTLLD 301
Db 219 FRRLQSGS--PNCFWASVSVAEGRRRAVELGRNLNCLNSDEBLIHLCKEKKQELID 276

QY 302 ATNNTPGFLAYSSL-RLSYLPDPGKNIITDDMYKLVRDGKYASVPVIGDQNDGTTIFGL 360
Db 277 VEWNV---LPFDSIFRFSVPVIDGEFFPTSLMSLNSGNPKKTQILLGVNKGDSFFLL 333

QY 361 -----SSLNVTNAQARAYFKQSFTHASDAEIDLMAAYPQDITQGSPPDTGVNAL 412
Db 334 YGAPGFKDSEKISREDFMGSVKLSVPHANDLGLDAVTLQY-----TDMDDNNIGIKR- 388

QY 413 TPQFKRISAVLGLDAFIHARRYFLN---HFQGGTKYSFLSKQLSGL---PINGTTHANDI 466
Db 389 -----DGLDDIVGDHNVICPLMFVNKYTKFGNGTYLFFNHRASNLVWPEWGVHGVET 444

QY 467 VMQDYLLGSGSVIYNN-----AFIAFATDLDPNTA-GLLVNWPKYTSSQ 510
Db 445 ---EFVFGPLVKELNYTAEEBALSRIMHYWATFAKTGNPNPHEPQSKWPLFTTKEQ 500

RESULT 4
US-08-348-920-2
; Sequence 2, Application US/08348920
; Patent No. 5695750
; GENERAL INFORMATION:
; APPLICANT: Doctor, Bhupendra P.
; APPLICANT: Maxwell, Donald
; APPLICANT: Saxena, Ashima
; APPLICANT: Radic, Zoran

```

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; APPLICANT: Taylor, Palmer
; TITLE OF INVENTION: Compositions for Use to Deactivate
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John F. Moran
; STREET: Off. of Command Judge Adv., HQ USAMRDC, Fort
; CITY: Frederick
; STATE: MD
; COUNTRY: US
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/348,920
; FILING DATE: 25-NOV-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: doc348,920
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-7807
; TELEFAX: 301-619-7714
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 575 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; US-08-348-920-2

Query Match 17.1%; Score 488.5; DB 1; Length 575;
Best Local Similarity 30.2%; Pred. No. 5.8e-39;
Matches 163; Conservative 76; Mismatches 195; Indels 105; Gaps 24;

QY 22 GDTITGLNAINAEFLGIPFAEPVGNLRFKDP---VPYSGSLNGQKFTSYGSPSCMQNP 78
Db 17 GTRVPVLSHSIS-AFLGIPFAEPVGNMFRPEPKPWSGVWNASTY----PNNCQQV 71

QY 79 EGTFEENLGTALDLVMSQKVFQAVLPQSEDCLTINV-----VRPPTKAGANLPVLMWIF 134
Db 72 DEQFPFGSG-----SEMNPNNREMSDCLYLNIVPSPRKST-----TWVVIY 116

QY 135 GGGFEIGSPTIPPPAQWTKSVLMGKH-----IIHVAANYRVASWGFLA--GDDIKAG 186
Db 117 GGGFYSGSSTL-----DVYNGKYLAYTEEVVLVSLSYRVGAFGLALHGSQ---EA 164

QY 187 SGNAGLKDOORLGMQWADNIAGFGDPKSVTIIFGSAGSMVLCILWINDGNTYKGPL 246
Db 165 PGNVGLLDORLQWALQVHDNIQFFGDPKVTIIFGSAGSAGVGMHIL-----SPGSRDL 218

QY 247 FRAGIMQSGAMVPSDP---VDGTYGNEIYDLFVSSAGCGSASDK--LACLRASASDTLLD 301
Db 219 FRRLQSGS--PNCFWASVSVAEGRRRAVELGRNLNCLNSDEBLIHLCKEKKQELID 276

QY 302 ATNNTPGFLAYSSL-RLSYLPDPGKNIITDDMYKLVRDGKYASVPVIGDQNDGTTIFGL 360
Db 277 VEWNV---LPFDSIFRFSVPVIDGEFFPTSLMSLNSGNPKKTQILLGVNKGDSFFLL 333

QY 361 -----SSLNVTNAQARAYFKQSFTHASDAEIDLMAAYPQDITQGSPPDTGVNAL 412
Db 334 YGAPGFKDSEKISREDFMGSVKLSVPHANDLGLDAVTLQY-----TDMDDNNIGIKR- 388

QY 413 TPQFKRISAVLGLDAFIHARRYFLN---HFQGGTKYSFLSKQLSGL---PINGTTHANDI 466

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QY 86 LKLTALDLVMSKVFQAVLPQSEDCLTINNVPRPGTKAGANLPVMLWIFGGFEGISPTI 145
Db 119 PNREL-----SEDCLYLN-VMTYPRTPTPTVLMWYGGGFYSGASL 161
QY 146 FPPAQMTKSVLMGKHIIH-----VANVYRVSAGFLAGDDIKAEKSGNAGLKQORLGM 199
Db 162 -----DVGDFPLVQAERTVLVSMYRVGAFGLALPGSR-EAPGNVGLLQORLAL 211
QY 200 QWVADNIAGFGDPKSVTIFGESAGSMVLCHLIWNGDNTYKGLPLFRAGIMQSGAMVP 259
Db 212 QWVQENVAAGFGDPTSVTLFGESAGASVGMHLL-----SPSRGLFHRAVLQSGA--P 263
QY 260 SDPVDTGTG-----NEIYDLFVSSAGC-----GSASDKLACLRASSDITLDATNN 305
Db 264 NGPW-ATVGMGEARRATQLAHL-----VGCPPGGTGGNDTELVACLRTPAQVLV---NH 315
QY 306 TPGFLAYSSL-RLSYLPRPDGKNITDDMYKLVRDGKYASVPVLIIGDQNDGTIF----- 358
Db 316 EHWLVPQESVFRFSPVVDGDFLSDTPEALINAGDFHGLQVLGVVVDKDEGSYFLVYGAP 375
QY 359 GLSSLN--VTTNAQARAYFKQSFIIHASDAEIDTLMAAY-----POD---ITQSPFDITGV 408
Db 376 GFSKDNESLISRAEFLAGVRVGPQVSDLAEEAVVLHYTDLWHPEDPARLREALSDVVDG 435
QY 409 LNALTPQFKRISAVLGDIAFIHAR--RYFLNHFG-----GTYKSFSLKQLSGLPT- 457
Db 436 HNVVCP-----VAQLAGRLAAQARVYAYVFEHRASTLSWPLMWGVPHGYEIEFIFGIPLD 491
QY 458 -MGTFHANDIVMODYLLGSGSVIYNNAFIATATLDLPNTA--GLLVNPKYTSQQ 510
Db 492 PSRYTAEEKIPAQRLLM-----RYWANFARTGDPNEPRDPKAPQPPYTAGAQ 539

RESULT 7

US-08-814-095-4
; Sequence 4, Application US/08814095
; Patent No. 6025183
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KOHN & ASSOCIATES
; STREET: 30500 No. 6025183thwestern Highway, Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: U.S.
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814,095
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N.
; REGISTRATION NUMBER: 38,972
; REFERENCE/DOCKET NUMBER: 2391.00066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 600 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-814-095-4
Query Match 15.8%; Score 452; DB 3; Length 600;
Best Local Similarity 29.1%; Pred. No. 2.5e-35;
Matches 156; Conservative 83; Mismatches 179; Indels 118; Gaps 26;
QY 35 AFLGIPFAEPVGNLRFKDP---VPYSGSLNGKFTSYGSPCMQ-----QNPETGTFEEN 85
Db 62 AFLGIPFAEPVGNLRFKDP---VPYSGSLNGKFTSYGSPCMQ-----QNPETGTFEEN 118
QY 86 LKLTALDLVMSKVFQAVLPQSEDCLTINNVPRPGTKAGANLPVMLWIFGGFEGISPTI 145
Db 119 PNREL-----SEDCLYLN-VMTYPRTPTPTVLMWYGGGFYSGASL 161
QY 146 FPPAQMTKSVLMGKHIIH-----VANVYRVSAGFLAGDDIKAEKSGNAGLKQORLGM 199
Db 162 -----DVGDFPLVQAERTVLVSMYRVGAFGLALPGSR-EAPGNVGLLQORLAL 211
QY 200 QWVADNIAGFGDPKSVTIFGESAGSMVLCHLIWNGDNTYKGLPLFRAGIMQSGAMVP 259
Db 212 QWVQENVAAGFGDPTSVTLFGESAGASVGMHLL-----SPSRGLFHRAVLQSGA--P 263
QY 260 SDPVDTGTG-----NEIYDLFVSSAGC-----GSASDKLACLRASSDITLDATNN 305
Db 264 NGPW-ATVGMGEARRATQLAHL-----VGCPPGGTGGNDTELVACLRTPAQVLV---NH 315
QY 306 TPGFLAYSSL-RLSYLPRPDGKNITDDMYKLVRDGKYASVPVLIIGDQNDGTIF----- 358
Db 316 EHWLVPQESVFRFSPVVDGDFLSDTPEALINAGDFHGLQVLGVVVDKDEGSYFLVYGAP 375
QY 359 GLSSLN--VTTNAQARAYFKQSFIIHASDAEIDTLMAAY-----POD---ITQSPFDITGV 408
Db 376 GFSKDNESLISRAEFLAGVRVGPQVSDLAEEAVVLHYTDLWHPEDPARLREALSDVVDG 435
QY 409 LNALTPQFKRISAVLGDIAFIHAR--RYFLNHFG-----GTYKSFSLKQLSGLPT- 457
Db 436 HNVVCP-----VAQLAGRLAAQARVYAYVFEHRASTLSWPLMWGVPHGYEIEFIFGIPLD 491
QY 458 -MGTFHANDIVMODYLLGSGSVIYNNAFIATATLDLPNTA--GLLVNPKYTSQQ 510
Db 492 PSRYTAEEKIPAQRLLM-----RYWANFARTGDPNEPRDPKAPQPPYTAGAQ 539

RESULT 8

US-08-975-084-1
; Sequence 1, Application US/08975084
; Patent No. 6258780
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: FRIEDMAN, Alon
; APPLICANT: SEIDMAN, Shlomo
; APPLICANT: KAUFER, Daniela
; TITLE OF INVENTION: A METHOD AND COMPOSITION FOR ENABLING
; TITLE OF INVENTION: PASSAGE THROUGH THE BLOOD-BRAIN-BARRIER
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 No. 6258780thwestern Hwy., Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: US
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,084
; FILING DATE: 11-NOV-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N.

```
;
; REGISTRATION NUMBER: 38,972
; REFERENCE/DOCKET NUMBER: 2391.00082
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 600 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
;
US-08-975-084-1

Query Match 15.8%; Score 452; DB 3; Length 600;
Best Local Similarity 29.1%; Pred. No. 2.5e-35;
Matches 156; Conservative 83; Mismatches 179; Indels 118; Gaps 26;

QY 35 AFLGIPFAEPVGNLRFKDP---VPYSGSLNGQKFTSYGPSQMQ-----QNPEGTFEEN 85
Db 62 AFLGIPFAEPVGNLRFKDP---VPYSGSLNGQKFTSYGPSQMQ-----QNPEGTFEEN 85
QY 86 LGKTALDLVMSQKVFQAVLPQSEDCLTINNVVRP---PGTKAGANLPMVLWIFGGGFEIGSPTI 145
Db 119 PNREL-----SEDCLYLN-VWTPPRPTSPTPLVLIWYGGGFGYSGASL 161
QY 146 FPPAQWTKSVLMGKHIIH-----VAVNRYVASMGFLAGDDIIKAEGSGNAGLKDQRLGM 199
Db 162 -----DVIDGRFLVQAERTVLVSMNRYVGAFFLALPGSR-EAPGNVGLLDQRLAL 211
QY 200 QWVADNIAGFGDPSPKVTIFGESAGSMVSLCHLIWNGDNTYKGLPLFRAGIMQSGAMVP 259
Db 212 QWVQENVAAFGGDPTSVTLFGESAGASVSLHLIL-SFGSHS-----LFTRAILQS 252
QY 260 SDVPDGTG---NEIYDLFVSSAGC-----GSASDKLACLRSSASDITLDAATNN 305
Db 264 NGPW-ATVGMGARRATQLAHL-----VGCPPGGTGNDTELVALCLRTPAQLV---NH 315
QY 306 TPGFLAYSSL-RLSYLPRPDGKNITDDMYKLVDRGKYASVPVLIIGDQNDGTFI----- 358
Db 316 EHWLVPQESVFRFSFPVVDGDFLSDTPEALINAGDFHGLQVLGVWVXDEGSYFLVYGAP 375
QY 359 GLSSLN--VTTNAQARAYFKQSFIIHASDAEIDTLMAAY-----POD---ITGSPDPTGV 408
Db 376 GFSKDNESLISRAEFLAGVVRGVQPQVSDLAEEAVVLHYTDLWHPEDPARLREALSDVVGD 435
QY 409 LNALTPQFKRISAVLGDLAFIHAR--RYFLNHFQ-----GTYKGFSLKQLSGLPI- 457
Db 436 HNVVCP-----VAQLAGRLAAQGARVYAVYFEHRASTLSWPLWMGVPHGYEIBFIFGILD 491
QY 458 -MGTTHANDIVMDYLLGGSGSVIYNNAFIATATDLPNTA--GLLVNMPKYTSSQ 510
Db 492 PSRNTAEBEKIFAQRLM-----RYWANFARTGDPNEPRDPKAPQWPPTTAGAQ 539

RESULT 9
5215909-11
; Patent No. 5215909
; APPLICANT: SOREQ, HERMONA
; TITLE OF INVENTION: HUMAN CHOLINESTERASE GENES
; NUMBER OF SEQUENCES: 13
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/572,911
; FILING DATE: 15-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 87,724
; FILING DATE: 21-AUG-1987
; APPLICATION NUMBER: 875,737
; FILING DATE: 18-JUN-1986
; SEQ ID NO:11:
; LENGTH: 602
5215909-11

Query Match 15.8%; Score 452; DB 6; Length 602;
Best Local Similarity 29.5%; Pred. No. 2.5e-35;
Matches 158; Conservative 82; Mismatches 190; Indels 106; Gaps 25;

QY 22 GDTITGLNAINAEAFGLIPFAEPVGNLRFKDPVPYSGSLNGQKFTSYGPSQMQQNPEGT 81
Db 50 GGTVT-----AFLGIPYAQPPLGRLRFKKQPSLTKWSDIWNATKYANSCC-QNIDQS 100
QY 82 FEENLGKTALDLVMSQKVFQAVLPQSEDCLTINNVVRP--PGTKAGANLPMVLWIFGGGFEI 140
Db 101 FPGFHG-----SEMNNTDLSDECLYLVNWIAPAKPK---NATVLIWYGGGQQT 148
QY 141 GSPTIFPPAQWTKSVLMGK-----HIIHVAVNYRYVASWGFAGDDIIKAEGSGNAGLKD 194
Db 149 GTSSL-----HVDGKFLARVERVIVSMNRYVGALGFALWPG-NPEAPGNMGLFD 198
QY 195 QRLGMQWADNIAGFGDPSPKVTIFGESAGSMVSLCHLIWNGDNTYKGLPLFRAGIMQS 254
Db 199 QQLALQWQKNIAAPGPNKSVTLFGESAGASVSLHLIL-SFGSHS-----LFTRAILQS 252
QY 255 GAMVPSDVPDGTG---GNEIYDLFVSSAGC---SASDKLACLRSSASDITLDAATNNTPGL 310
Db 253 GSFNAPWAVTSLYEARNETLNL-AKLTCGSRNETETI IKLRNKDPQBEIL---LNEAFV 308
QY 311 AYSS-RLSYLPRPDGKNITDDMYKLVDRGKYASVPVLIIGDQNDGTFI-----GLSSL 363
Db 309 PYGTPLSVNFGPTVDGDFLTMDPDLLELQFKTKQILVGVNKGDEGTAFVYGAFFGSKD 368
QY 364 N--VTTNAQARAYFKQSFIIHASDAEIDTLMAAY-----PODITGSPDPTGVNLALT 413
Db 369 NNSIITRKEPQEGGLKIPFGVSEFGKESILFHYTDWDDQRPENTREALGDVVDYNYFIC 428
QY 414 P--QFKRISAVLGDLAFIHARRYFLNHFQGGTKYSLFKQLSGLPIMGTFHANDIWMODY 471
Db 429 PALEFTKXFSWGNNAFF---YVFEH-----RSSKLWPPEWVMGVMHGYEI---EF 472
QY 472 LLG-----SGSVIYNNAFIATATDLPNTA--TAGLLVNMPKYTSSQ 510
Db 473 VFGLPLERRDNTYKABEILSRIV--KRWANFAKYGNFNETQNNSTSWPVFKSTEQ 526

RESULT 10
5215909-11
; Patent No. 5215909
; APPLICANT: SOREQ, HERMONA
; TITLE OF INVENTION: HUMAN CHOLINESTERASE GENES
; NUMBER OF SEQUENCES: 13
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/572,911
; FILING DATE: 15-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 87,724
; FILING DATE: 21-AUG-1987
; APPLICATION NUMBER: 875,737
; FILING DATE: 18-JUN-1986
; SEQ ID NO:11:
; LENGTH: 602
5215909-11

Query Match 15.8%; Score 452; DB 6; Length 602;
Best Local Similarity 29.5%; Pred. No. 2.5e-35;
Matches 158; Conservative 82; Mismatches 190; Indels 106; Gaps 25;

QY 22 GDTITGLNAINAEAFGLIPFAEPVGNLRFKDPVPYSGSLNGQKFTSYGPSQMQQNPEGT 81
Db 50 GGTVT-----AFLGIPYAQPPLGRLRFKKQPSLTKWSDIWNATKYANSCC-QNIDQS 100
QY 82 FEENLGKTALDLVMSQKVFQAVLPQSEDCLTINNVVRP--PGTKAGANLPMVLWIFGGGFEI 140
Db 101 FPGFHG-----SEMNNTDLSDECLYLVNWIAPAKPK---NATVLIWYGGGQQT 148
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Qy	141	GSPTIFPPAQWTVKSVLMGK-----HIHVAVNVRVASWGFLAGDDIKAEGSGNAGLKD	194
Db	149	GTSSL-----HVDGKFLARVERIVVSMNRYVGALGPGLAWPG-NPEAPGNMGLFD	198
Qy	195	QRLGQWQVADNIAGFGGDPKVTIFGESAGSMVLCHLIWDDGNTYKGKPLFRAGIMQS	254
Db	199	QQLALQWQKNIAPFGGNPKSVTLFESAGAAASVLIHLT-SPGSHS-----LFTTALIQS	252
Qy	255	GAMVPSPDVGTY--GNEIYDLFVSSAGCG--SASDKLACLRASASDILLDATNTPGFL	310
Db	253	GSPNAPWAVTSLYEARNRTLNL-AKLTCGRESNETEIIKLRNKPQEIL---LINEAFV	308
Qy	311	AYSS-LRLSYLPRPDGKNITDDMYKLVRDGKVASVPVIIGDONDGTTF-----GLSSL	363
Db	309	PYGTPLSVNFQFTVDGDFLTOMPDILLELGQPKTQILVGVNKNDEGTAFLVYGAPGFSKD	368
Qy	364	N-V-VTTNAQARAYFKQSFIHASDAEIDTLMAAY-----PQDITQGSPPDVTGVNALT	413
Db	369	NNSIITRKEPQEGLUKIFPGVSEFGKESILFHYTDWDDQRPENTREALGDVVGDYNFIC	428
Qy	414	P--QFKRISAVLGDLAFTHARRYFLNHPQGGTKYSFLSKQSLGSLPMGTFTHANDIWMQDY	471
Db	429	PALEFTKKFSEGNNAFF---YYFEH-----RSLKLPWPPEMGMVHGYEI---EF	472
Qy	472	LLG-----SGSVIYNNAFIAPATOLDPN-TAGLLVNNPKYTTSSQ	510
Db	473	VFGLEPLERRDNYTKAEIILRSIV--KQWAMPKYGNEPNETONNSTSWPFGKSTQ	526

RESULT 11

US-07-732-962A-2
; Sequence 2, Application US/07732962A
; Patent No. 5248604
; GENERAL INFORMATION:
; APPLICANT: Fischer, Meir
; TITLE OF INVENTION: EXPRESSION OF ENZYMATICALLY ACTIVE
; TITLE OF INVENTION: RECOMBINANT HUMAN ACETYLCHOLINESTERASE

Query Match 15.8%; Score 452; DB 1; Length 614;
Best Local Similarity 29.1%; Pred. No. 2.5e-35;
Matches 156; Conservative 83; Mismatches 179; Indels 1

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35 AFLGIPFAEBPPVGNLRKDP---VPYSGSLNGQKFTSVGPSCMQ---QNPGTFFBEN 85
Db AFLGIPFAEBPPVGNLRKDP---VPYSGSLNGQKFTSVGPSCMQ---QNPGTFFBEN 118
Qy LGKTALDLVMQSKVFQAVLPQSEBCLTINVVRPCTKAGANLPMVLWTFGGGFBIQSPTI 145
Db PNRRL-----SEDCLYLN-VMTYPRETSTPTPLVLIWYGFGFYGSASLS 161
Qy FPPAQMVTKSYLMGKHIIH-----VAVNYRVASWGFLAGDDDKAEGSGNAGLKDQRLLM 199
Db DVEDGRFLVQAERTVLVSNNYRVGAFFLALPGSR-EAPGNVGLLDORLAL 211
Qy QWADVADTAGGGDSKTYITGESAGSMVLCILLWNDCDNTRYKGKPLFRAGIMQSGAMVP 259
Db QWQOENAAAFGGDTSVTLFGEESAGAASVGMHLL-----SPPSRGLFHRAVLQSGA--P 263
Qy SDPDVGTYG-----NEYDLFVSSAGC-----GSASKLAACLRASSSDTLILDATNN 305
Db NGPW-ATVNGEARRRATQLAHL-----VCPPGTGGNDTELVACLRTPAQVLV---NH 315
Qy TPQFLAYSSL-RLSYLRPRPGKNITDDMYKLVRDGKYASVPIIGDONDEGTIF----- 358
Db EHWVLPQESVRFPSFPVMDGDFLSDTPEALINAGDFHGLQVLGVGWKDGSYFLVYGAP 375
Qy GLSLNL-VTTNAQARAYFKQSFTHASDAEDITLMAAY-----POD-----ITQGSFDTGV 408
Db GFSKONESLISRAEFELAGVRVGVQPQVSDLAABAVLHYTDWLHPEDPARREALSDVVGD 435
Qy LNALTPQFKRISAVLGDLAFTHAR--RYFLNHFOG-----GTKYSFLSKQLSGLPI- 457
Db HNVVCP-----VAQLAGRLAAGARVYAYVEHRASTLSWPWMGVPHGYEIEFIIGIPLD 491
Qy -MGTGHANDIVWDYLGSGSVIYNNAFIAPATLDPNTA--GLLVNMPKYTSSSQ 510
Db PSRNYTABEKIFAQRLM-----RYWANPARTGDPNEPRDKPAQPPVYTAGAQ 539

RESULT 12
US-08-370-156-2
; Sequence 2, Application US/08370156
; Patent No. 5932780
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reising, Ethington, Barnard & Perry
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: US
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,156
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-307 (Mulford)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 689-4071
; TELEFAX: (810) 689-4071
; INFORMATION FOR SEQ ID NO: 2:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-370-156-2

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Best Local Similarity 29.1%; Pred. No. 2.5e-35;
Matches 156; Conservative 83; Mismatches 179; Indels 118; Gaps 26;

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QY 119 PNREL-----SEDCLYLN-VMTYPYPRPTSPTPVLVWIVGGFYGSGASL 161
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QY 162 -----DVTGDFLQVQAEFTVLSMNYRVGAFGLALPGSR-EAPGNVGLLDQRLAL 211
QY 200 QWVADNIAGFGDPSKVTIFGESAGSMVSLCHLIWNGDNTYKGLPLFRAGIMQSGAMVP 259
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 212 QWQENVAAGFGDPTSVTLFSGAGASVGMHLL-----SPPSRGLFHRVAVLQSGA--P 263
QY 260 SDPVGVTVG-----NEIYDLFVSSAGC-----GSASDKLACLRASSDTLDDATNN 305
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 264 NGPW-ATVGMGEARRRATQLAHL-----VCGPPGGTGGNDTELVACLRTPAQVLV--NH 315
QY 306 TPGFLAYSSL-RLSYLPRPDGKNITDDMYKLVRDCKYASVPVLIIGDQNDGTIF----- 358
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QY 316 EHWLVPQESVFRFSFVPVVDGDFLSDTPEALINAGDFHGLQVLGVVKGDEGSYFLVYGAP 375
QY 359 GLSSLN--VTNQAQARYFKQSFIHASDAEIDTLMAAY-----PQD-----ITQGSPPDTGV 408
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
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RESULT 13

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US-08-446-100-19
; Sequence 19, Application US/08446100
; Patent No. 6001625
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GENERAL INFORMATION:

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; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
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CORRESPONDENCE ADDRESS:

```
; ADDRESS: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
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COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: Broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
; US-08-446-100-19

Query Match 15.8%; Score 452; DB 3; Length 614;
Best Local Similarity 29.1%; Pred. No. 2.5e-35;
Matches 156; Conservative 83; Mismatches 179; Indels 118; Gaps 26;

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QY 119 PNREL-----SEDCLYLN-VMTYPYPRPTSPTPVLVWIVGGFYGSGASL 161
QY 146 FPPAQWVTKSVLMGKHIIH-----VAVNYRVASWGLAGDDIKAEGSGNAGLKDQRLGM 199
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QY 316 EHWLVPQESVFRFSFVPVVDGDFLSDTPEALINAGDFHGLQVLGVVKGDEGSYFLVYGAP 375
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QY 436 HNVVCP-----VAQLAGRLAAQARVYAVFEHRASTLSWPLVMGVPHGYEIEFIFGIPLD 491
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RESULT 14

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; Sequence 21, Application US/08446100
; Patent No. 6001625
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GENERAL INFORMATION:

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; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
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Search completed: September 17, 2005, 07:51:48
Job time : 45 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 17, 2005, 07:49:54 ; Search time 172 Seconds
(without alignments)
1287.764 Million cell updates/sec

Title: US-09-943-857A-4
Perfect score: 2864
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Scoring table: BLOSUM62
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Searched: 1812044 seqs, 404927589 residues
Total number of hits satisfying chosen parameters: 1812044

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/ECT_NEW_PUB.pep.*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
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- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2864	100.0	547	10 US-09-943-857-4	Sequence 4, Appli
2	2588	90.4	547	10 US-09-943-857-10	Sequence 10, Appl
3	2513	87.7	549	20 US-11-061-894-2	Sequence 2, Appli
4	2513	87.7	549	20 US-11-061-233-2	Sequence 2, Appli
5	2495	87.1	547	10 US-09-943-857-8	Sequence 8, Appli
6	2434	85.0	547	10 US-09-943-857-6	Sequence 6, Appli
7	2396	83.7	547	10 US-09-943-857-2	Sequence 2, Appli
8	1170.5	40.9	561	15 US-10-369-493-4236	Sequence 4236, Ap
9	674.5	23.6	612	9 US-09-875-353-4	Sequence 4, Appli
10	674.5	23.6	612	16 US-10-193-452-30	Sequence 30, Appl
11	672.5	23.5	574	13 US-10-023-515-4	Sequence 4, Appli

12	672.5	23.5	574	15	US-10-674-636-4	Sequence 4, Appli
13	664	23.2	585	9	US-09-934-323-4	Sequence 4, Appli
14	664	23.2	585	16	US-10-193-452-56	Sequence 56, Appl
15	484	15.9	576	18	US-10-503-643-3	Sequence 3, Appli
16	484	15.9	576	18	US-10-503-691-4	Sequence 4, Appli
17	482	16.8	574	9	US-09-748-739A-21	Sequence 21, Appl
18	482	16.8	574	14	US-10-032-233-48	Sequence 48, Appl
19	482	16.8	574	16	US-10-413-432-48	Sequence 48, Appl
20	482	16.8	574	16	US-10-324-466-48	Sequence 48, Appl
21	477	16.7	574	9	US-09-748-739A-23	Sequence 23, Appl
22	477	16.7	574	14	US-10-032-233-50	Sequence 50, Appl
23	477	16.7	574	16	US-10-413-432-50	Sequence 50, Appl
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26	459	15.0	574	14	US-10-032-233-49	Sequence 49, Appl
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28	459	15.0	574	16	US-10-324-466-49	Sequence 49, Appl
29	459	15.0	574	18	US-10-728-723-188	Sequence 188, App
30	458	16.0	574	18	US-10-728-723-164	Sequence 164, App
31	457	16.0	530	18	US-10-728-723-204	Sequence 204, App
32	457	16.0	574	18	US-10-728-723-178	Sequence 178, App
33	457	16.0	574	18	US-10-728-723-180	Sequence 180, App
34	457	16.0	574	18	US-10-728-723-184	Sequence 184, App
35	457	16.0	765	18	US-10-728-723-202	Sequence 202, App
36	456	15.9	574	14	US-10-032-233-40	Sequence 40, Appl
37	456	15.9	574	16	US-10-413-432-40	Sequence 40, Appl
38	456	15.9	574	16	US-10-324-466-40	Sequence 40, Appl
39	456	15.9	574	18	US-10-728-723-32	Sequence 32, Appl
40	456	15.9	574	18	US-10-728-723-74	Sequence 74, Appl
41	455	15.9	574	9	US-09-748-739A-8	Sequence 8, Appli
42	455	15.9	574	18	US-10-728-723-42	Sequence 42, Appl
43	455	15.9	574	18	US-10-728-723-114	Sequence 114, App
44	455	15.9	574	18	US-10-728-723-186	Sequence 186, App
45	454	15.9	574	18	US-10-728-723-40	Sequence 40, Appl

ALIGNMENTS

RESULT 1
US-09-943-857-4
; Sequence 4, Application US/09943857
; Publication No. US20030124701A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Jei-Fu
; APPLICANT: Lee, Guan-Chiun
; APPLICANT: Tang, Shye-Yue
; TITLE OF INVENTION: RECOMBINANT CANDIDA RUGOSA LIPASES
; FILE REFERENCE: 08919-066001
; CURRENT APPLICATION NUMBER: US/09/943,857
; CURRENT FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Candida rugosa
; US-09-943-857-4

Query Match 100.0%; Score 2864; DB 10; Length 547;
Best Local Similarity 100.0%; Pred. No. 1e-250;
Matches 547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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; Publication No. US20030124701A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Jei-Fu
; APPLICANT: Lee, Guan-Chiun
; APPLICANT: Tang, Shye-Jye
; TITLE OF INVENTION: RECOMBINANT CANDIDA RUGOSA LIPASES
; FILE REFERENCE: 08919-066001
; CURRENT APPLICATION NUMBER: US/09/943,857
; CURRENT FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Candida rugosa
US-09-943-857-10

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RESULT 3
US-11-061-894-2
; Sequence 2, Application US/11061894
; Publication No. US20050188439A1
; GENERAL INFORMATION:
; APPLICANT: McCutchen, Billy F.
; APPLICANT: Abad, Andre R.
; TITLE OF INVENTION: Methods for Enhancing Insect Resistance
; FILE REFERENCE: 035718/286812
; CURRENT APPLICATION NUMBER: US/11/061,894
; CURRENT FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: 60/546,845
; PRIOR FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: 60/546,533
; PRIOR FILING DATE: 2004-02-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Lipase from C. cylindracea
US-11-061-894-2

Query Match 87.7%; Score 2513; DB 20; Length 549;
Best Local Similarity 87.5%; Pred. No. 7.8e-219;
Matches 470; Conservative 32; Mismatches 35; Indels 0; Gaps 0;
Qy 11 LGSVPTAKLANGDTITGLNAINAEFLGIPPAEPVGNLRFKDPVPSGSLNGQKFTSYG 70
Db 13 VAAAPTATLANGDTITGLNAINAEFLGIPPAEPVGNLRFKDPVPSGSLNGQKFTSYG 72
Qy 71 PSCMQONPEGTFEENLGKLTALDLVMQSKVFOAVLPQSEDCLTINVRPPGTAGANLPM 130
Db 73 PSCMQONPEGTYEENLPKAAALDLVMQSKVFEAVSPSEDCLTINVRPPGTAGANLPM 132
Qy 131 LWIFGGFEIGSPTIPPPAQMVTKSVLMGKHIIHVAVNVRVASWGFLAGDDIKAGSGNA 190
Db 133 LWIFGGFEIGSPTIPPPAQMTKSIAMGKPIIHVSVNVRVSSWGFLAGDDIKAGSGNA 192
Qy 191 GLKQRLGQWADVADNIAGFGDPBSKVTIEGESAGNSVLCHLIWNGDNTYKGLPFRAG 250
Db 193 GLKQRLGQWADVADNIAGFGDPBSKVTIEGESAGNSVMCHLMNDGNTYKGLPFRAG 252
Qy 251 IMQSGAMVPSDPVDGTYGNEIYDLFVSSAGCGSASDKLACLSASDITLLDATNNTPGFL 310
Db 253 IMQSGAMVPSDAVDGIYGNEIFDILLASNAGCGSADKLACLRGVSSDTLEATNNTPGFL 312

OTHER INFORMATION: Consensus sequence
US-10-023-515-4

Query Match 23.5%; Score 672.5; DB 13; Length 574;
Best Local Similarity 34.9%; Pred. No. 1e-51;
Matches 195; Conservative 76; Mismatches 195; Indels 93; Gaps 18;

QY 35 AFLGIPFAEPPVGNLRFKDPVPY-----SGSLNGQKFTSYGSPCMQONPEGTFEENLGKTA 90
DB 19 SFLGIPYAEPPVGNLRFKAPQPYKEPWSVDLDA---TKYPPSCLQDDDFGFSLSL-KVA 74

QY 91 LDLVMSKVFOAVLPQSEDCLTINVRPGTKAGANLPMWLIFGGGPFIGSPTTIPPAQ 150
DB 75 LKMLSLGMNKLVLGKLSLCLVLYNVPKNTKPNKLPVMVWIHGGGFMGSGHSLPLSL 134

QY 151 MYTKSVLMGKHIIHVAVNVYRVASWGLAGDDIKAEKSGNAGLKDORLGMQWADNIAAG 210
DB 135 YGESLARGNVIVSINIRLGLPLGFLSTGDDKLPFGSGNYGLDORLALKWQDNIAPG 194

QY 211 GDPKVTIFGESAGSMVLCILWNGDNTYKGLFRAGIMQSGA-----MVPDPVDG 265
DB 195 GDPNSVTIFGESAGASVSLLLSNGDNPSSKGLFHRAISQSGSALSPWAIQESNAR 254

QY 266 TYGNEIYDLFVSAGCG--SASDKLACLRSSASDITLLDNTNTPGFLAYS-----SLRLS 318
DB 255 GRAKELARLL---GCNETSSSELDDCLRSKSAELLEATRS---FLLFYVVPFLPLFLA 307

QY 319 YLPRPDGKN-----ITDDMYKLVRGKYASVPIIGDQNDGCTIFGLSSLVNTTNAQAR- 372
DB 308 FGPVVDGDDAPFAPIEDPEELKEGKFADVPYLGVTKDEGGYFAAMLLNASSGDEB 367

QY 373 -----AYFKOSFIHASDA-----EIDTLMAAYPQDITQGGSPFDGTGVLNALT 414
DB 368 KKETNPVWLELLKVLFFYASEALNIKMDLDLADKLVLEKPGDVDDFS-----VES 418

QY 415 QPKRISAVLGDLAP-----IHARR-----YFLNHFGGKYKFLSKQLSGLPLM 458
DB 419 RKPNLQDMLTDLFKCPTRVAADLHAKHGGSPVYAYVFDHPASFGIGQFLAKRVDP-BFG 477

QY 459 GTFHANDI--VWQDYLL-----GSGSVIYNNAFATADLDPN--TAGLLVNW 502
DB 478 GAVHGEIFFVFGNPLLEKQLYKATEEBEKSSTMMYANFANFAGTGNPNNGTNGLVVW 537

QY 503 PKYTSSSQSGNNLMINAL 521
DB 538 PKYTSEEQKYSLLILLTTI 556

RESULT 12

US-10-674-636-4
Sequence 4, Application US/10674636
Publication No. US20040086922A1
GENERAL INFORMATION:
APPLICANT: Curtis, Rory A. J.
APPLICANT: Silos-Santiago, Inmaculada
TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
FILE REFERENCE: 10448-122001
CURRENT APPLICATION NUMBER: US/10/674,636
CURRENT FILING DATE: 2003-09-29
PRIOR APPLICATION NUMBER: US/10/023,515
PRIOR FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 60/256,369
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: 60/279,508
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 574
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Consensus sequence
US-10-674-636-4

Query Match 23.5%; Score 672.5; DB 15; Length 574;
Best Local Similarity 34.9%; Pred. No. 1e-51;
Matches 195; Conservative 76; Mismatches 195; Indels 93; Gaps 18;

QY 35 AFLGIPFAEPPVGNLRFKDPVPY-----SGSLNGQKFTSYGSPCMQONPEGTFEENLGKTA 90
DB 19 SFLGIPYAEPPVGNLRFKAPQPYKEPWSVDLDA---TKYPPSCLQDDDFGFSLSL-KVA 74

QY 91 LDLVMSKVFOAVLPQSEDCLTINVRPGTKAGANLPMWLIFGGGPFIGSPTTIPPAQ 150
DB 75 LKMLSLGMNKLVLGKLSLCLVLYNVPKNTKPNKLPVMVWIHGGGFMGSGHSLPLSL 134

QY 151 MYTKSVLMGKHIIHVAVNVYRVASWGLAGDDIKAEKSGNAGLKDORLGMQWADNIAAG 210
DB 135 YGESLARGNVIVSINIRLGLPLGFLSTGDDKLPFGSGNYGLDORLALKWQDNIAPG 194

QY 211 GDPKVTIFGESAGSMVLCILWNGDNTYKGLFRAGIMQSGA-----MVPDPVDG 265
DB 195 GDPNSVTIFGESAGASVSLLLSNGDNPSSKGLFHRAISQSGSALSPWAIQESNAR 254

QY 266 TYGNEIYDLFVSAGCG--SASDKLACLRSSASDITLLDNTNTPGFLAYS-----SLRLS 318
DB 255 GRAKELARLL---GCNETSSSELDDCLRSKSAELLEATRS---FLLFYVVPFLPLFLA 307

QY 319 YLPRPDGKN-----ITDDMYKLVRGKYASVPIIGDQNDGCTIFGLSSLVNTTNAQAR- 372
DB 308 FGPVVDGDDAPFAPIEDPEELKEGKFADVPYLGVTKDEGGYFAAMLLNASSGDEB 367

QY 373 -----AYFKOSFIHASDA-----EIDTLMAAYPQDITQGGSPFDGTGVLNALT 414
DB 368 KKETNPVWLELLKVLFFYASEALNIKMDLDLADKLVLEKPGDVDDFS-----VES 418

QY 415 QPKRISAVLGDLAP-----IHARR-----YFLNHFGGKYKFLSKQLSGLPLM 458
DB 419 RKPNLQDMLTDLFKCPTRVAADLHAKHGGSPVYAYVFDHPASFGIGQFLAKRVDP-BFG 477

QY 459 GTFHANDI--VWQDYLL-----GSGSVIYNNAFATADLDPN--TAGLLVNW 502
DB 478 GAVHGEIFFVFGNPLLEKQLYKATEEBEKSSTMMYANFANFAGTGNPNNGTNGLVVW 537

QY 503 PKYTSSSQSGNNLMINAL 521
DB 538 PKYTSEEQKYSLLILLTTI 556

RESULT 13

US-09-934-323-4
Sequence 4, Application US/09934323
Patent No. US20020150910A1
GENERAL INFORMATION:
APPLICANT: Curtis, Rory A. J.
TITLE OF INVENTION: 33410, A NOVEL HUMAN CARBOXYLESTERASE
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
FILE REFERENCE: 10448-081001
CURRENT APPLICATION NUMBER: US/09/934,323
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/226,774
PRIOR FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 585
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Consensus sequence
US-09-934-323-4

Query Match 23.2%; Score 664; DB 9; Length 585;
Best Local Similarity 34.0%; Pred. No. 6.3e-51;


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Db 3 VATNNVLCKVRGVEKNTDNGSQSVYFGLGIPYAEPPVGNLRKAPQPKYKPMWDLDA- 61
Qy 65 KFTSYGPSQCMQNPBTGTEBENLKTALDLVMSQKVFQAVLPQSEDLCTINVRPPTKAG 124
Db 62 ---TKYPPSCLODDRGFSLSDL-KVALKMLSLGNKLVGLKLSLSEDLCTINVRPPTKRN 118
Qy 125 ANLPWMLTFGGGPFISPTIPPPQMVTKYSLVMGKHIIHVAIVNRVAVSWGFLAGDDIKA 184
Db 119 SKLPVWVTHGGGPFMGSGHSLPLSLYDGESLAREGNIVVSVINRVLPLGLSLTGDDKL 178
Qy 185 EGSNGAG-LKQORLGMOWADNIAAGFGDPSKVTIFGESAGSMVSLCHLIWNDDNTYKG 243
Db 179 PGSGNYGLLDORLALKWQDNIAPFGDPNSVTIFGESAGAASVSLLLSNGSDNPPSS 238
Qy 244 KPLFRAGIMQSCA-----MVPDPVDGTGNYBIYDLFVSSAGCG--SASDKLACLRSSAS 296
Db 239 KGLFHRAISQSGSALSPWAIQESNARGRAKELARLL---GCNETSSSELLDCLRSKA 294
Qy 297 DTLIDATNTPGFLAYS-----SLRLSYLPRPDGKN-----ITDDMYKLVDRDGKVASVPV 346
Db 295 BELLEATRS---FLLFXYVPFLPLFLAFGPPVVDGDAPEAFIPEDPEELIKEGKPADVPY 351
Qy 347 IIGDQNDCTIFGLSLNVTNTAQR-----AVFKQSFTHASDA-----EI 387
Db 352 DTLMAAYPDITQGSPPDTGVNLALTPQPKRISAVLGLDAF-----IHARR----- 433
Qy 388 DTLMAAYPDITQGSPPDTGVNLALTPQPKRISAVLGLDAF-----IHARR----- 433
Db 412 DKVLEKYPGDDVDFP-----VESRKPNIQDMLTDLLFKCPTFVAADLHAKHGGSVPV 462
Qy 434 ---YFLNHFQGGTKYFSLKSLGSLPIMGTFFHNDI---VWQDYLL-----GSGS 477
Db 463 YAYVFDHPASFGIGQFLAKRVDP-BFGGAVHGDEIFFVFGNPLKQYKATEBEKSSS 521
Qy 478 VIYNNAFTAFATDLPN--TAGLLVNWPKYTSQSGNNLMXMINAL 521
Db 522 KTMNYWANFAKTGNPNNGTNSGLVWVWPKYTSSEOKYSLILLITTI 567

RESULT 15
US-10-503-643-3
; Sequence 3, Application US/10503643
; Publication No. US20050176117A1
; GENERAL INFORMATION:
; APPLICANT: Robyn Joyce Russell
; APPLICANT: Rama Heidari
; APPLICANT: Alan Devonshire
; APPLICANT: Susan Jane Dorrian
; APPLICANT: John Graham Oakeshott
; TITLE OF INVENTION: Degradation of hydrophobic ester pesticides and toxins
; FILE REFERENCE: 69-04
; CURRENT APPLICATION NUMBER: US/10/503,643
; PRIOR FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: PCT/AU02/00114
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Torpedo californica
US-10-503-643-3

Query Match 16.9%; Score 484; DB 18; Length 576;
Best Local Similarity 30.6%; Pred. No. 1.3e-34;
Matches 160; Conservative 73; Mismatches 192; Indels 98; Gaps 23;

Qy 35 AFLGIPFAEPVGNLRFKDP---VPYSGSLNGQKFTSYGSCMQONPEGTFFENLGTAL 91
Db 30 AFLGIPFAEPVGNLRFKDP---VPYSGSLNGQKFTSYGSCMQONPEGTFFENLGTAL 91
Qy 92 DLVMSQKVFQAVLPQSEDLCTINVRPPTGKAGANLPVWMLWIFGGGPFISPTIFPPAQ 150
Db 92 DLVMSQKVFQAVLPQSEDLCTINVRPPTGKAGANLPVWMLWIFGGGPFISPTIFPPAQ 150
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Db 82 -----SEMNPNREMSDCLYLNIVWPSRPRKSAT---VMLWIYGGGYSGSSTL----- 128
Qy 151 MVTKSLVMGKH-----LIHVAVNVRVASWQFLA--GDDIKAEKSGNAGLKQORLGMOWV 202
Db 129 -----DVYNGKYLAYTEEVVLSLSYRUGAFGLALHGSQ---EAPGNMGLLDORVALQWV 181
Qy 203 ADNIAGFGDPSKVTIFGESAGSMVSLCHLIWNDDNTYKGKPLFRAGIMQSGAMVPSDP 262
Db 182 HDNIQFGGDPKVTITLFGESAGRASVGMHIL-----SPGSRDLFRRALQSGS--PNCP 233
Qy 263 ---VDGTYGNEIYDLFVSSAGCGSASDK--LACLRASASDILLDATNTPGFLAYSSL-R 316
Db 234 WASVSAEGRRAVELRENLCNLSRDLIQCLREKKPQELIDYEMNV---LPFDSIFR 290
Qy 317 LSYLPRPDGKNITDDMYKLVDRDGKVASVPVLIIGDQNDGTTIFGL-----SSLNVTTN 368
Db 291 FSPVVIDGEPFPTSLESMLNAGNFKTKQIILGVNKDEGSPFLLYGARGFSGKDSKISR 350
Qy 369 AQARAYFKQSFTHASDAEIDTLMAAYPODITQGSPPDTGVNLALTPQPKRISAVLGLDAF 428
Db 351 EDFMSGVKLSVPHANDLGLDAVTIQLY---TDWMDNNGIKNR-----DGLDDIVGNHNV 401
Qy 429 IHARRYFLN---HFQGGTKYFSLKSLGSL---PIWGTFFHNDIYVWQDYLLGSGSVIYNN 482
Db 402 ICPLMHFYNKYTKFGNGTYLYFFNHRASNLVWPEWMMGVHGYEI---BFFVGLPLVKELN 458
Qy 483 -----AFTAFATDLPNTA--GLLVNWPKYTSQSSQ 510
Db 459 YTAEEALSRIMHYWATFATGNPNRPHSQSKWPLFTTKEQ 501
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Search completed: September 17, 2005, 08:04:13

Job time : 174 secs

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